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Pred. No. is the number of results predicted by chance to have a score atteator than or equal to the score of the result being printed. and is derived by analysis of the total score distribution

SUMMARIES	

Result	s. Section	Match Areno	Query Query Match Length DB		10	Doser iption
	P6.4	10 10 10 10 10 10 10 10 10 10 10 10 10 1	402	16	R79931	Foreing acylalucos
t.	691	\$2.2	402	16	R74928	Porcine acylglucus
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л	94	ے ش	532	20	Y39296	Alkaline Bacillus
'n.	£ 6.		883	2	Y44935	Corn sulphate perm
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S. pueumoniae deri Chlamydia trachoma	Plant territin.	Streptococcus phen	Alpha-amylase prot	Alpha-amylase vari	Alpha amylase vari	Keratinocyte growt	Newt keratineeyte	Hok Like newt Fork	Fibroblast growth	Chlamydia pueumoni	C. pheumonide	C. pheumoniae 73 k	 pnoumoniae poly 	Human apoptin asso	Alpha amylase vari	Wild type Termanyl	Wild type It						Bacillus sp.	Alpha amy ase vari		-	_		al Flu	- - - -	kat alpha-d subuni
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RESULT R79931

R79931 Standard: Protein: 402 AA

09-MAY-1996 (first entry)

/note- "wild type Asp subord, with Glu^n Misc-difference 28909-SEP-1994; 25-MAR-1994; mutant Poreine: acylylucosamine 2 epimerase: N-acetylmannosamine: N-acetylheuraminic acid: renin-binding; enzymatic production: Porcine acylalucosamine-2-epimerase mutant W09526399-A1 Misc-difference Misc-difference Sus scrota. 24-MAR-1995; 94JP-0216333. 94JP-0056271. 95Wo-JP00541 /not.e-317 /note "wild type Ser substd. with Ard" Location/Qualitiers /note-"wild type Glu substd. with Glu' "wild type His substd. with Tyr'

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Best Local Similarity 34.8%; Pred. No. 8
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                                                                                                                                                          MOD526399 AL
                                                                                                                                                                                                                                                                           Poreline; acylethicosamine-2 epimetase; N acetylmannosamine; N acetylmentaminic acid; renin-binding; enzymatic production
                                                                                                                                                                                                                                                                                                                                                                            Porcine acylalucosamine 2 epimerase
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                                   24 MAR 1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant acylidheosamine 2 epimerase with remin binding activity - useful in enzymic production of N-acetyl:mannosamine and N-acetyl:neuraminic acid
 Χυ/
                                                                       Porcine: acylqlucosamine-2-epimerase; N-acetylmannosamine; N-acetylneuraminic acid; renin binding; enzymatic producti
                                                                                                                                                                                                          k79930 standard; Protein; 419
                             Sus scrota.
                                                          mutant.
                                                                                                                  Porcine acylqlucosamine-2-epimerase mutant
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with renin-binding activity. A2P can be used for the enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2: Pages 53-54; 74pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09 SEP 1994;
25-MAR-1994;
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meuraminic acid; renin binding; enzymatic production;
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tive 71; Mismatches 151; Indels 4
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                                                                                                                           WQFAVFYNRLE - - PKPQWLEIARHGADFLARHGR - - DQDGNWYFALDQEGKPLRQPYNVF 117
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Pred. No. 1.3e-59;
**smatches 163;
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                                                                                                                 page, and an iso-electric point of about 5. The amylase has optimum activity at about 55 degrees C and pH 9.5, and can be used in the production of improved detergents, e.g. laundry and hard surface cleaning detergent compositions. It is also useful in the production of sweeteners and ethanol from starch and also in the conventional starch-converting
                                                                                                                                                                                            This is a Bacillus species alpha-amylase amino acid sequence. The alpha-amylase is derived from a strain of Bacillus. The preferred strain is Bacillus sp. NGIMB 40916. The mature protein sequence and the polynucleotide coding for the mature protein sequence are specifically claimed. The protein has a molecular weight of 55kD, as determined by SD claimed. The protein has a molecular weight of 55kD, as determined by SD claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y39296;
                        cardboard. The new alpha-amylase may also be used in modifying starch
the presence of alkaline fillers such as calcium carbonate, in the
textile industry for textile desizing, and in beer-making during the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ethanol; starch conversion; liquetaction; saccharitication; pulp; paper; cardboard; liquocellulosic material; textile desizing; alkaline;
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                                                                      pulp, paper and cardboard, from starch reinforced
                                                                                         also be used in the production of lignocellulosic materials, such
                                                                                                      processes such as liquelaction and saccharification. Alpha-amylase may
                                                                                                                                                                                                                                                                                                                        Novel alpha-amylase enzymes derived from
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/note- "The mature protein is specifically claimed"
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p0121 offine Or and p0128 optic209 from cbu10, cooler, p0004, p0004, p0004, p0128 libraries, respectively. It has 80.28 sequence identity to speciabolus staphianus sulphate permeaso(di 1907270). This sequence is used as a probe to isolate other plant sulphate.
                                                                                                                              The present ambino acid sequence is the corn sulphate permease, a sulphate assumblation protein. This sequence is from a contia composed of closes cholo.pknu6.2.bi0, ccolo.pknu6.12, ccolo.pknu6.2.b, ccolo.pknu6.2.bi0, ccol
                                                                                                                                                                                                                                                                                              Claim 6; Page 89 41; Pypp: English
                                                                                                                                                                                                                                                                                                                                                                 homologous proteins, in producing transpense plants
                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid traducuts encoding sulfate assimilation proteins in plants and seeds useful as probes for isolating cDNAs and genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N PSDB; Z50481
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hos 65; Conservative
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; Pred. No. 0.28;
35; Mismatches 84; Indels 1
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and as markers of traits linked to the denes. This is useful to plant
breeding and to construct chimeric genes, used to create transcenic
plants with altered levels of sulphate permease. The sulphate permease
                              New Streptococcal protein, useful as a vaccine, for diagnostic of
                                                                                                Gilbert CEG,
                                                                                                                                                                                                                                                                            W0200006747 A2
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                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae; vaccine; screening; protein antique; antibacterial; antiinflammatory; meningitis; infection; diagno
                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae type 4 protein sequence #17
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                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae.
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Similarity 19.1%; Pred. No. 0.53;
62; Conservative 46; Mismatches
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pneumococcal diseases and for screening agents capable of antaphizing or inhibiting expression of the protein

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of anlagonising, inhibiting or interlering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. A05591 to A05614 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y81501 to Y81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. A05407 to A05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful for the diagnostic assays. The proteins and nucleotides can be useful for the
                                                                                                                                                                                                                                              02-OCT-1998
                                                   Mise-difference
                                                                                                          Streptococcus
                                                                                                                                                                                                       Streptococcus pneumoniae SP0048 protein.
                                                                                                                                                                                                                                                                                                                     W55100 standard;
                                                                                                                                                detection; pneumonia; otitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGLMREAVTPTGEFVDSFEGR----LLNPGHGIEAMWFMMDIAQRSGDR------QLQEQ 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGNWYFALDQEGKPLRQPYNVESDCFAAMAFSQYALASGAQEAKATALQAYNNVLRRQHN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vfdt-----hyqsw----fyikadanyaenewl---kqqddyfylksqgymaksewve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---HLETTLVALAKGHQAFGQEKCW-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         659 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 42; Mismatches 109; Indels 159;
                                                                                                                                                                                                                                          (lirst entry)
                                                                                                            pneumoniae
               /note- "encoded by ARK"
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       - FGYLNRRGEV 360
                                                                                                                                                                                                                                                                                                                       Protein; 368
                                   /label- unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----qikykdyyfksggylltsqwinqayvnasgakvqqqwlfdkqyq 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.3%; Score 92.5; DB 18.8%; Pred. No. 0.56;
                                                                                                                                                 media; meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----OWERVHDYAWSHFADDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347
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24-MAY-2000 (first entry)

Streptococcus pneumoniae protein sequence ID204 · 4117.1.

RESULT 9 Y81667

Y81667 standard; Protein; 678

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $ \times 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 \times 0 \times 0 0 \times 
     В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antiquens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 coupled to a toxin or the skin of the skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of intection e.g. pneumonia, otilis media or meningitis. Probes based on the public acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a protein from Streptococcus preumoniae The nucleic acid sequence encoding the Streptococcus preumoniae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 65; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi GH,
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353 tsidqyrvndnqew
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                                                                                                    364 LK------GGKW
                                                                                                                                                                                                                                                                                                                  304 LWWVHLETLVALAKGHQATGQEKCWQWFERVHDYAWSHFADPEYGEWFGYLNRRGEVLLN
                                                                                                                                                                                                   sswyyl-----nsngsmkvngwfg------vggkwy-yvntsgelavn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 AA;
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19.7%; Pred. No. 0.26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matchess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection and diagnosis of S. pueumoniae. The protein sequences are also useful for screening an agent capable of antagonisting, hibibiting or interfering with the function of expression of the proteins in which the agent is useful for freatment or prophylaxis of S. pueumoniae intection and meningities. A0559 to A05644 represent primers used to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated from Streptococcus pneumoniae. A05407 to A05540 represent
specifically claimed nucleofide sequences isolated from S. pneumoniae.
The sequences have antibacterial and antinilammatory properties.
The protein sequences, and fragments of them, are useful as immunosons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6: Page 89: 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exemplification of the present inzention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 IIII. 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae; vaccine; screening; protein antiden; antibacterial; antifullammatory; meningitis; intection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic assays. The proteins and nucleotides can be useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y81501 to Y81679 represent specifically claimed protein sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or inhibiting expression of the protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and/or antiques. The nucleotide sequences can be used in vaccines
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274 ydshsqawyytksqqymtanewiwdkeswtylksdqkiaekewvydshsqawyytksqqy
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                                                                                                                                                                                                                                             156 PROOYEKSYPOTREEKSLAVEMILAN LITLEMENLLEFTTVEEVLAOTVREVMIDETDEE 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                    47 VEDTEKETMLONROVWOEAVEYNRLE PKPOWLETARHGAD ...
                                                                                                                                                                                                                                                                                                                                                         96 DGNWYFALDQEGKFLRQPYNVFSDCFAAMAFSQYALASGAQEAKATALQAYNNVLRRQHN 155
                                                                                                                 ATAVVIALLEYAWDEEF GGTFYFILDROGH PPOOLEWDOKIW
                                                                           swlyikenenya dkewitenghyyylksaaymaanewiwdkeswlyiktdakmaekewv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109; Indels 159; Gaps
                                        OWFERVHDYAWSHFADDEY 47
                                                                                                                                                                                                                                                                                                                                                                                                                                      FLARBGRDQ 95
                                                                                                                                                                                                 QLQEQ 264
                                                                                                                                                                                                                                         170
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126 urngeisady

4 HRROELAGGYYGALHODVLDFWEKYSLDROGGGYFTGLDRKGOVFDIDKFIWLGNRGVWg 6.4

46; Mismatches 124; Indels 182;

-----tieawtkidipgranty---sdikwrwyhidavdwdasia

172

Query Match Best Local Similarity

4.1%; 19.8%;

Score 88;

DB 17; Length 484;

Conservative

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                                                                                         dependency. The variants can also have increased alpha-amylolyric activity (especially alpha values in these variant alpha-amyloses also possess improved specificity to a particular substrate. These variant alpha-amylases also possess improved specificity to a particular substrate, and/or improved
                                                                                                                                                                                                                                                   mutagenesis of the DNA sequences encoding the parent alpha amylases represented by W12955, W12956, R81835 and R81836. W12137 W12140, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bisdard trantzen H. Borchert I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha amylase: determent: thermal stability; oxidation stability; enzymes calcium ton dependency; alpha amylolytic activity; washing composition;
              The alpha amylase variants can also be used in papermaking and beer making processes. These variants can also be used in the production
                                                    specificity with respect to cleavage of substrate. These sequences can be used in determent and washing compositions, and for textile designing
                                                                                                                                                                        thermal stability (such as at temperatures in the range of 40.70 degree
Celeius), and/or exidation stability, and/or reduced calcium ion
                                                                                                                                                                                                                                 W12144 are specifically variants of the alkaphilic Bacillus strain NCTB
                                                                                                                                                                                                                                                                                            variants of the
                                                                                                                                                                                                                                                                                                            W12098-W12144 represent alpha amylase variants of the invention
                                                                                                                                                                                                                                                                                                                                                     Example 3; ; lllpp; English.
                                                                                                                                                                                                                                                                                                                                                                                         Alpha amylase variants - with
stability and reduced calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPT: 1996-471424/37.
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29 - SEP - 1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03 FEB 1995;
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                    (BERG/) BERG I.
                                                15-JAN-1996;
                                                                         15-JAN-1447;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the LAMAN coding sequence (see 191094). A claimed method for diagnosing or screening for bam comprises detecting the presence or absence of bam causing mutations in the LAMAN gene; another point
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This alycosylated polypeptide comprises a mutant borine lysosomal alpha-mannosidase (LAMAN) that causes bowine alpha-mannosidosis ban) in Galloway. The RZZHH mutation results from a point mutation of the LAMAN coding sequence (see 191994). A claimed method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation causing bam in Angus and related breeds of cattle has also
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27-MAR-1998 (first entry)
                                           W26683;
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Query Match 4.1%; Score 87.5; Dibest Local Simularity 17.5%; Pred, No. 3.6;
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                                                                                                                                                                  the specification)
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                                                                                                                                                                                                                 the sequence for the £4211 mutant alpha mannosidase was
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                              Alpha sub unit polypoptide of human beta 2 integrin—used to identity potential antiinflammatory agents, for the treatment graft afteriosclerosis, inflammatory bowel disease, asthma, e
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23-DEC-1993;
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Mise-difference 1128
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                                                                                              WPI: 1995 240603/31
                                                                                                                       Gallatin WM.
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      Page 138-142; 172pp; English
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Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A rat cDNA clone was isolated from a spleen library in lambda-qtl0 on the basis of homology to the human integrin alpha-d subunit dene. RAME and PCR amplification were used to obtain the complete rat alpha-d sequence given in 091715. Rat alpha-d I domain/human
                                                                                                                                                                                                                                                                                    cell adhesion: phagocytosis: diabetes: atherosclerosis: multiple sclerosis: asthma; psoriasis: lung inflammation: acute respiratory distress syndrome: rheumatoid arthritis:
                                                                                                                                                                         Location/Qualifiers
Mise-difference 474
                                                                                                                                                                                                                                                                        hybridoma:
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                                                                                                                                                                                                                                                                                                                                          Beta 2 integrin alpha d subunit; rat; cell migration
                                                                                                                                                                                                                                                                                                                                                                            Rat beta 2 integrin alpha d subunit.
                                                                                                                                                                                                                                                                                                                                                                                                          24 FEB-1998 (first entry)
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 55-FEB-1996;
                                 24-FEB-1997;
                                                                  28 - AUG - 1997
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                                 97WO-US02713.
                                                                                                                                                  /note- "encoded by ACY"
1128
                                                                                                                                    /note- "encoded by TYC"
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20.2%; Pred. No. 4.5;
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Hest Local Similarity 20.2%; Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identifying antibodies or Other compounds that modulare alpha detivity or which modulate the interaction between alpha deand a liquid, for treating or preventing diseases in which macrophages implicated. A monoclonal antibody that is specific for ratelpha 4 subunit, and which is secreted by hybridoma 199M (AICC HB 12058), is claimed. It may be used to modulate alpha decivity, interlers with human alpha deand treat or prevent diseases such as type I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library. Alpha d is involved in cell migration, phagocytosis and cell-cell interaction. Recombinant alpha d polypeptides can be expressed in transformed host cells for use in assays for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybridoma 199M and antibody secreted by it—specific for new
beta2 integrin subunit, useful to detect subunit in cells and
modulate its activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This polypeptide comprises the rat homologue of a novel human beta 2 integrin subunit, designated alpha d (see W23049). Its sequence was deduced from a cDNA clone (see T79257) isolated from a spleen
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                                             G------GKWKGCFHVP--RALWLCAETL 386
                                                                                     prhqhtgkvviftgearhwrpk-----sevrgtgigsytaaslesvdvdidgsxdlvli
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qaphyyeqtrqqqvsv1pvpqvrqrwqceatl 511
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                                                                                                                                       -HQATGQ-----EKCWQWFERVHDYAWSHFADPEYGEWFGY-----LNRRGEVLLNLK-365
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Bost Local :
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23 DEC
                                                                                                                                                                                                                                                                                  The present sequence represents rat alpha d. The present invention describes: (1) an antibody that specifically binds alpha A which is a beta 2 integrin alpha-subunit polypeptide; (2) a monoclonal antibody as in (1); (4) an anti-lidiotype antibody specific for the monoclonal antibody of (2). (4) a hybridoma cell line producing the monoclonal antibody of (2). Antibodies specific for alpha d can be used in immunohistochemical analysis to localise alpha d to subcellular comportiments or individual cells within tissues. Substances that modulate alpha d binding (which may include antibodies) can be used to treat diabotes, atherosclerosis, multiple selerosis, asthma, pseriasis, lung
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                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Column 14 (150; 106pp; English.
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SUMMARIES

Result		A.tono				
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24	79.5	3.7	1155	_	US-08-485-618-46	46,
25	79.5	3.7	1155	<u>_</u>	US-08-362-652-46	46,
25	79.5	3.7	1155	2	US-08-605-672-46	46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MARU, ISAFUMI
APPLICANT: CHIA, YASUHIRO
APPLICANT: TSUKADA, YOJI
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FASTSEQ Version 1.6 CURRENT APPLICATION DATA:
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STREET: 620 Newport Center Drive 16th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MARU, ISAFUMI
APPLICANI: OHIA, YASUHIRO
APPLICANI: ISUKADA, YOJI
TELECOMMUNICATION INFORMATION: TELEPHONE: 714 760-0404
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                           NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DSECKET NUMBER:
                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 QEKDPEYGEWFGYLNREGKVALTIKGGPFKGCFHVPRCLAMCEEMLSALLS 499
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                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        COMPOTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLIY: Newport Beach
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                                                                                                                                                                APPLICATION NUMBER:
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N terminal
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34.8%; Pred. No. 7.4e 65
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: Patent No. 5994105
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Best Local Similarity
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MOLECULE TYPE: poptide
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/006,021
                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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TELEX:
                                                                                                      SOFTWARE: FastSEQ Version 1.5
                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                    CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                            ADDRESSEE: Knobbe, Martens, Olson & STREET: 620 Newport Center Drive 16
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CLASSIFICATION:
RIOR APPLICATION DATA:
                                           FILING DATE:
                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                         TBM Compatible
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RESULT 5

18-08-553-704A-3

/ Sequence 1, Application US/08554703A

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MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
                                                                                          APPLICANT: MARU, ISAFUMI
APPLICANT: OHFA, YASUHIRO
APPLICANT: TSUKADA, YOJI
TITLE OF INVENTION: EPTMERASE
NUMBER OF SEQUENCES: 9
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FILING DATE: 30-NAV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Altiman, Daniel E
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOOKET NUMBER: TELECOMMUNICATION INFORMATION: 714-760-0404
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                                                                        CORRESPONDENCE ADDRESS
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TYPE: a
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th F
CITY: Newport Beach
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TELEFAX: 714-760-9502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 WOFAVEYNRLE--PKPQWLEIARHGADFLARHGR--DQDGNWYFALDQEGKPLKQFYNVF 117
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35.0%; Pred. No. 1.54-64;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COUNTRY: U STATE

U.S.A.

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16th Floor

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                                                                                                                                                                  Sequence 5 Application MS/09006021
Patent No. 5991105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 145; Conservative 71; Mismatches 151; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 81.1%; Score 668; D8-1; Best Local Similarity (5.6%; Pred. No. 4.8c-62;
                                                                                                                                         GENERAL INFORMATION:
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               APPLICANT: MARU, ISARIMI
APPLICANT: OHTA, VASHIMI
THILE OF INVENTION: EPIMERASE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: poptide ERACMENT TYPE: N terminal
CORRESTONDENCE ADDRESS
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NAME: ATTHAIN, Dathiot E
REGISTRATION NUMBER: 44,115
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                                                                                                                                                                                                                                                                                                          34.8 HQFRDFEYGEWFGYLNQEGKVALTIKGGFFKGCFHVPRCLAMGEQIL 394
                                                                                                                                                                                                                                                                                                                                                         40 SHFAOFEYJEWFGYLNERGEVLLNLKGGKWKGCFHVPRALMLCAETL 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 714 750 9502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 31.1%; Score 668; DB 2; Length 419; Hest Local Similarity 35.6%; Pred. No. 4.3e 62; Matches 145; Conservative 71; Mismatches 151; Indels 40;
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FRAGMENT TYPE: N (erminal
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PRIOR APPLICATION DATA:
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                                             340 SHEADPEYGEWEGYLNERGEVLLNIKGGKWKGCEHVPRALWIGAETI 386
                                                                                               288 EBGGLEYEQDADDLCETQLEWNMKLWWPHTEAMTAFLMGYRDSGDFALLNLEYOVAEYTE 347
                                                                                                                                          280 EFGGTEYFIDROGHPPOOLEWDOKLWWYHLEILVALAKGHQATGOEKCWOWFFRVHDYAW
                                                                                                                                                                                                                                       221 AVIPTGEEVDSTEGRIINEGHGIEAMWEMMOIAQRSGDRQIQEQAI AVVINTIEYAWDE 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 WMYCKLYKITERFKKVELLIDAAKAGGEFILSYAKVAPPGKKGAFVLTQDGKFVKVQKT1F 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: simple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5
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HOFRDPEYGEWFGYLNOEGKVALFIKGGPFKGCFHVPRCLAMCBOIL 394
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GENERAL INFORMATION:
APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RETERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: EPIMERASE
297 DADNECPTQLEWAMKLWWPHSEAMIAFLMGYSDSGDPVLLRLFYQVAEYTERQFRDPEYG 356
                                       289 DROGHPPOOLEWDOKLWWVHLETLVALAKGHOATGOERCWOWFERVHDYAWSHFADDEYG 348
                                                                                  2 17
                                                                                                                                                                     183
                                                                                                                                                                                                               177
                                                                                                                                                                                                                                                  12 \pm SECFYTMAMNELWRATGEVRYQTEAVEMMDQIVHWVQEDASGLGRPQLQGAPAAEPMAVP- 182
                                                                                                                                                                                                                                                                                             118 SINTHAAMAHSQYALASGAQEAKATALQAYNNVLR-RQHNPKGQYEKSYPGTRPLKSLAVP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Knobbe, M
SIREET: 620 Newport
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
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                                                                                                                                                                                                                                                                                                                                     63 WMYCRLYKTFEKFRHAQLLDAAKAGGEFLLRYARVAFPGKKCAFVLTREGRFVKVQRT1F 122
                                                                                                                                                                                                                                                                                                                                                                            62 WOFAVEYNRLE: PKPQWLEIARHGADELARHGR--DQDGNWYFALDGEGKPLKGPYNVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : ASc/leafer1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 714-760-9502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X37134.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 RRQELAQQYYQALHQD---VLPFWEKYSLDRQGGGYFTCLDRKGQVFDTDKFIWLQNRQV 61
                                                                                                                                                                                                                                                                                                                                                                                                                      3 KERETLÓAWKERVGÓELDRVVAFWMEHSHDOEHGGFFTCLGREGRVYDDLKYVWLOGRÓV 62
                                                                                PGCLGRQQNPGHTLEAGWELLRHCIRKGDPELRAHVIDKELLLPFHSGWDPDHGGLFYFQ 296
                                                                                                                        DSFEGRLINPGHGIEAMWFMMDIAQRSGDRQLQEQAI-AVVLNTLEYAWDEEFGGIFYFL 288
                                                                                                                                                                 MMILLNILVEGI.-----GEADEELAGKYAELGDWCARRILDHVQRDGQAVLENVSEGGKEL 236
                                                                                                                                                                                                        MILANLTLEMEWLLPPTTVEEVLAQTVREV-----MTDFLDPEIGLMREAVTPTGEFV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92660
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620 Newport Center Drive 16th F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.0%; Score 645; DB 1; Length 417; 34.7%; Pred. No. 1.1e-59;
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US-09-006-021-2
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: Parent No. 5994105
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                                                                                                                                                                                                                                                                                                                                Query Match (0.0%; Score 645; DE 2; Lebath 417; Best Local Similarity 84.7%; Pred. No. 1.1e 59; Matches 138; Conservative 75; Mismatches 164; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MAKU, ISAFUMI
APPLICANT: OHIA, YASUHIRO
APPLICANT: TSUKADA, YUJI
TIILE OF INVENTION: EFIMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide FRAGMENT TYPE: N-terminal
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ALLORNEY/AGENI INFORMATION:
NAME: Altman, Daniel E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
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  183 MMLLNLVEQL----
                                    177 MILANUTLEMENULPPITVEEVLAQTVREV----- MIDFLDPETGLMREAVIPTGEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 EWFGYLSKEGKVALSTKGGFFKGGFHVPRGLAMGEEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
SIRANDEDNESS: single
ToPOLOGY: linear
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REGISTRATION NUMBER: 34
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                                                                                                                                                                63 WMYCRLYRIFERERHAOLLDAAKAGGEFILRYARVAPPGKKCAFVLIKDGREVKVORTIE 122
                                                                                                                                                                                                      62 WQFAVFYNRLE--PKPQWLEIARHGADFLARHGR--DQDGNWYFALDQEGKPLRQPYNVF 117
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                                                                                                                                                                                                                                                                   3 KERETLQAWKERVGQELDRVVAFWMEHSHDQEHGGFFTCLGREGRVYDLLKYVWLQGRQV 62
                                                                                SECFYTMAMNELWRATGEVRYQTEAVEMMDQIVHWVQEDASGLGRPQLQGAPAAEFMAVF 182
                                                                                                                      SDCFAAMAFSQYALASGAQEAKAIALQAYNNVLR-RQHNPKGQYEKSYPGTRPLKSLAVP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 amino acids
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-GEADEELAGKYAELGDWCARRILQHVQRDGQAVLENVSEGGKEL
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HS 08 485 518 55
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Fatent No. 5728533

        Query Match
        4.1%;
        Secret 87.5;
        DB 1;
        Length 1161;

        Host Local Similarity
        20.2%;
        Fred. No. 2.8;
        16.8;
        Indets 141

        Matches
        70;
        conservative
        49;
        Mismatches
        123;
        Indets 141

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                                                                                                                                                                                                                                                                                                MODEMIE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROOF APPLICATION DATA:
APPLICATION NUMBER: US 08/62/65/2
FILING DATE: 21 DEC 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,497
FILING DATE: 24 DEC 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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     161 EKSYPCTRPLKSLAVPMILANLILEMEWILLPP
                                                      155 FLIDGSGSINORDFAQMKD:
                                                                                                       101 FALLWEGKELL@PYNVESDCEAAMAESQYALLASGAWEAKATALWAYNNVLERWHNPKGQY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 DSEPTRILLNPCHCHEAMMEMMDTAQRSCDRQLQEQAT-AVVILNTLEYAWDEEFCGTFYFL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 DADNECPTQLEWAMKLWWPHSEAMTAFLMGYSDSGDPVLLRLEYQVAEYTFRQFRDPEYG 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERALING SYSTEM: POSTOS/MS DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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FILLING DATE: 5 AUG 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 233 Section CLIV: Chicago
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                                                                                                                                                                                                                                                                                                                                                                            TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: (8,659)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUDRESSEE: Marshall, O'Toole, Gerstein, Murray & Horun
STREET: 234 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMPGYLSREGKVALSTKGGPFKGGFHVPRGLAMGEEML 394
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                                                                                                                                                                                                                                                                                                                                                                                               1161 amino acids
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312 474 0448
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3ER: 27866/32797
                                                                                                                                                           49; Mismatches 123; Indels 141; Gaps
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Patent No. 5766850
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MOLECULE TYPE: protein
                                                                                                                                  TELEX: 25 8856
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APPLICANI: Van der Vieren, Monica

LITTE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Submnit
                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino aci
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ALIOKNEY/AGENI INFORMATION:
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COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-TOS/MS DOS
SOFTWARE: Pateutin Release #1.0, Version #1.25
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                                           TYPE: amino acid
topology: linear
                                                                                                                                                                                                                                                        REFERENCE/IFOKET NUMBER: 38,659
                                                                                                                                                                                                                                                                              NAME: Williams Jr., Joseph A. REGISTRAFION NUMBER: 38,659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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CTTY: Chicago
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FILING DATE: 5:AUG-1994
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                                                                                                                                                                                  TELEPHONE: $12,474-6300
TELEFAX: $12-474-0448
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: Patent No. 5817515
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GENERAL INFORMATION:
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                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTURNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFIWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TILLE GE INVENTION: NO. 5817515el Human
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 1
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                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               FILING DATE: 23-DEC-1993 PRIOR APPLICATION DATA:
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STREET: 23
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                                                           NAME: Williams Jr., Joseph A. REFERATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/286,889 FILING DATE: 5-AUG-1994
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERALING SYSTEM: PC-DOS/MS-DOS
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STATE: Illino
TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/605,672
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Mismatches 123; Indels 141; Gaps
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US-08-482-293A-55
; Sequence 55, Application US/08482293A
; Patent No. 5831029
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Matches 79; Conserv
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INFORMATION FOR SEQ 10 NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
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                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                           THILE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gallatin, W. Michael APPLICANT: Van der Vieren, Monica
                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                        FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 G-----GKWKGCFHVP--RALWLCAETL 386
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
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                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               COUNTRY:
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20.2%; Pred. No. 2.
                                                                                                                                                   US/08/482,293A
US 08/286,889
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FRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                        COMPUTER READABLE FORM:
                                                                                                                                                            NUMBER OF SEQUENCES: 114
ADDRESSE: Marshall, o'loole, Gerstein, Murray & Wordn
                                                                                                                                                                                                                          APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 588747801 Human 2 Integrin Alpha Subunit
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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                                                                                    COUNTRY:
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    COMPUTER
                       HEDIUM TYPE:
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                Floppy disk
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21 pec 1994
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US 08-944-363-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WILLIAMS IT., JOSEPH A.
KERISTRATION NUMBER: 38.659
REFERENCE/TO-KERT NUMBER: 27866/42684
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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FILING DATE: 23 DEC-1993
PRIOR APPLICATION DATA:
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480 GAPHYYEÇIKGGQVSVEPVPGVKGKWÇCEAIL 511
                                                                                                    426 PRHOHIGKVVIFTOEARHWRPK----- SEVRGTQ1GSYFGASLCSVDVDROGSXDLVL1 479
                                                                                                                                                  319 --HOATGO----EKCWOWEERVHDYAWSHEADBEYGEWEGY------LNRKGEVILLNLK 365
                                                                                                                                                                                                      375 SWS - GGAFLY- --- PPNTRPTFINMSQENVDMRDSYLGYSTAVAFWKGVHSIILGA 425
                                                                                                                                                                                                                                                         276 AWDEEFGGTEYFLDROGHPP----- QQLEWDQKLWWVHLETLVALAKG ------ 318
                                                                                                                                                                                                                                                                                                             418 GNE - AALRSTOROLOEKTEATEGTQSRSSSSEOHEMSQEGESSALTSDGEVLGAVGSE 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 EKSYEGIKELKSLAVEMILANLILEMEWILLER - --- LIVEEVI. - -
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                                                G-----KMKGCTHVP -KALWIJCAETL 386
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; Sequence 2, Application US/08446803; Patent No. 5824531

GENERAL INFORMATION:

APPLICANT:
APPLICANT:

ottrup, Helle Bisgard-Frantzen, ostergaard, Peter

Rahbek

US 08-446-804-2

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4.0%: Score 86; DB.

Best Local Similarity 20.0%: Pred. No. 1.1;

Natches 87; Conservative 48; Mismatches
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-08-446-803-2
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INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DISCRET NUMBER: 4157,204-US
FELECOMMUNICATION INFORMATION:
FELEPHONE: (212) 867-0123
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: Van Der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
NUMBER OF SEQUENCES: 5
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                                        455 -- NRRGEVLLNLKGGK 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/446,803
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                                                                                                                                                                                                                                                                                                                LAQTVREVMTSFLDPEIGLMREAVTPTGEFVDSFEGRLLNPGHGIEAM---WFMMDIAQR 255
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Sequence 2, Application US/08861837; Patent No. 5856164; GENERAL INDOCESS
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Best Local Similarity
Matches 87; Conserv
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Van Der Zee, Pia
Tille OF INVENTION: Alkaline Hacilius Amylase
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APPLICANT: Bisdard Frantzen, Henrik
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUFUMARE: Patentin Rollows...
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  32
                                      199 LAQTVREVMTDFLDFEIGLMREAVTFTGEFVDSFEGRLLNFGHGIEAM - - WEMMDIAQR 255
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ToPoLoGY: linear
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20.0%; Pred. No. 1.1;
Mismatches 127: Indels
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                                                                                                                                                                                                    --VESDCEAAMAESQYALASGAQEAKATALQAYNNVLERQ 153
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Title:
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Listing first 45 summaries
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VERSION KEYWORDS SoffRCE

AW551042.1 GT:7196470 EST.

ORGANISM

Mus musculus

house mouse

ACCESSION DEFINITION

AWS51042 614 bp. mRNA EST 02 ANG 2000 AWS51042 8 Morse ELZ.5 Female Mesonephros and Gonads CDNA Library Mus masculus CDNA Chone L0072008 47, mRNA sequences.

KETEKENST

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AUTHORS

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

COMMENT

Contact: George J. Karqul

Laboratory of Genetics

JUURNAI

denome wide expression profiling of mid destation placenta and embryo using a 15,000 monse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9142 (2000)

Lamaka.T.S., Jaradat,S.A., Lim,M.K., Karqul,G.J., Wang,X., Grahov,M.J., Pantano,S., Sano,Y., Fiao,Y., Nagaraja,R., Doi,H., Wood,W. LII, Becker,K.G. and Ko,M.S.H.

GLABOVAC

Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi: Mammalia: Entherma: Rodentia: Semuroquathi: Muridae: Murinae; Mus.

National Institute on Ading/National Institutes of Health 833 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

FEATURES.

POLYA Yes.

Plate: 10072 row: G column: 08 Seq prime: '21M18 Forward High quality sequence stop: 614

Email: edna dasum.gre.nia.nih.gov

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Obery Match (11.7%; Score 137.8; DB 23; Length 614; Hest Local Similarity 56.7%; Pred. No. 7.9e 42; Matches 275; Conservative 0; Mismatches 207; Endels 4; sdet: ()

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ligation mixture by chemical method. The library was constructed by xiaobong Wang."

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size selected by Gibco's Size Fractionation Column. The cDNAs were closed into Sall/NotI site of pSPokH plasmid vector. The DHIOR E. coli hast was transformed with the

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/note-"Vector: psporI (Gibco/BRL Life Technology):
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primer-adapter from GibcoBRL]
[5] pdAcTASTTCTAGNICGGARCGCCGTTTTTTTTTTTTTTTTTT" from

/Clone, Lib. "Mouse El2.5 Female Mesonophros and Gonads cDNA Library" $\,$

/clone-"L0072G08" /db_xre1-"taxon:10090" /strain "C57BL/6J" ∕organism "Mus musculus" Location/qualifiers

/lab_host-"DH108" /dev_stage="12.5dpc" /sex-"temale"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Systematic analyses of genes expressed in 3.5-dpc mouse blastocyst (The ERATO/Doi Project at Wayne State University)
[Inpublished (1997)
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Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C78078.1 GI:2518408
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Japan Science and Technology Corporation (JST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Hirofumi Doi
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/fissue_type-"blastocyst"
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                                                                                                                                                                                                                                                                                                                     Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishiqo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
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1 (bases 1 to 517)
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                                                                                                                                                                                                                                                                                                   Email: kazusudi cocoa.ocn.ne.jp
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                 /note-"Vector: p2L1; Site_1: Sal1; Site_2: Not1; Foly was deleted from a Not1 site"

1 146 c 158 q 96 t 5 others
                                                                                                                                                 /db_xref="taxon:9913"
/clone="E1K1013F07"
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                                                                                /dev_stage="letus"
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                                                                                                              451 Eckstein Medical Research Building lowa city, rel: 319-335-8250
                                                                                                                                                                                                                                                                                                                    97044477
                                           Email: msoares@blue.weeq.uiowa.edu
                                                                                                                                                                                                  University of Towa
                                                                                                                                                                                                                                 Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                         Contact: Soures,
                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                        discovery
                                                                                                                                                                                                                                                                                                                                                                                                                           Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Seluroquathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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The sequence tag present in the cDNA between the Not1 site and the
                                                                                       Fax: 319 335 9565
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/dev_stage="M30_CD4+ cells"
/lab_bost="SOLR_(kanamycin_resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Mus musculus"
/db_xref "taxon:10090"
/elone-"IMAGE:958903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Stratagone monse Teell 93/31]"
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Pred. No. 3.9e-28;
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ATGTGCCGCGGTGCCTGGCCATGTGCGAGCAGATTTT 112
                                                                                                                                                                                                                  TGAM/CAMGAGGAMAAGGTGGCCTTACCATCAAAGGAGGTCCTTTTAAAGGCTGCTTCC 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer: M13 Forward
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/lab_host-"DH10B (Lite Technologies)"
/note-"Vector: pf7T3D-Pac (Pharmacia) with a modified
/note-"Vector: pf7T3D-Pac (Pharmacia) with a modified
/note-"Vector: Site_1: Not 1: Site_2: Eco RI: Nic UI-R-Y0
| library is a subtracted library derived from an
| individually-tagged normalized whole-eye (minus the lens)
| library. The driver for the subtraction consisted of a
| pool of all previous libraries (UI-R-A0, UI-R-L1, UI-R-E0,
| pool of all previous libraries (UI-R-A0, UI-R-L1, UI-R-E0,
| pool of all previous libraries (UI-R-A0, UI-R-L1, UI-R-E0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligo-di track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-Y0) was constructed as follows: PCR applicated CDNA inserts from previous library clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UI-R-EL, UI-R-CO, and UI-R CL). The tag is a string of 8-5 nucleotides present between the Not 1 site and the
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/clone_lib="U1-R-Y0"
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                                                                     A1794002 532 bp mkNA EST Danio rerio cDNA 5' similar to 1036a08.yl Zebralish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:RNEP_RAT P51607 RENIN-RINDING PROTEIN ;, mkNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Entheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
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Ko,M.S.H., Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T.,
Gtahovac,M.J., Mason,S., Lim,M.K., Paonessa,P.D., Sauls,A.D. at
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Japan Science and Technology Corporation (JSI)
WBG Marive East 12F, 2-6 Nakase, Mihama·ku, Chiba 261-71, Japan
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/tissuc_type-"blastocyst"
/dev_stage="3.5-dpc"
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/clone-"J0001D11"
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 487
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Sequencing Center Clone distribution: Genome Systems, St. Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 into denomosystems.com) and Research Genetics, Hontsville, Alabama (web address: www.resgen.com) (email contact: info dresgen.com) and
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Institut ther Molekulare Genetik,Herlin), cDNAs for EST
analysis were selected following oligonucleotide
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: NCL-CGAP clone distribution information can be tound through the L.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael k
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 514)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1819201.1 G1:5438280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gener Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clNA Library Arrayed by: Gred Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencin, Center
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                                              Fatima Bonaldo.
a. 157 c. 12
                                                                                                                                                                                                                                                                                                                            Zhote "Graan: kidney: Vector: pTZTRCPac (Pharmacia) with a modified polylinker; Site_E: Not I; Site_E: Eco Ri. Plasmid DNA from the normalized library NCI CRAP Kid5 was prepared, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive
                                                                                                                                                                                     from a pool of 5,000 clones made from the same library (cloneIDs 132912-132584), 1471368 1472903 and
                                                                                             1492104-1493255). Subtraction by Bento Soares Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                        hybridization reaction. The driver was FCK amplified cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type "2 pooled tumors (clear cell type)"
/lab host "DHluB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NC1_cGAP_Kid12"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 CUCTUUMAGIIGAAGIIGAAGIGAAGITIIGGIGAUCACAGAGAGAAGATATGAIIGCI 284
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Local Similarity 55.0%;
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                                                                                                                                                                                                                                                                                                                                                        Email: msoares blue.weeg.uiowa.cdu

The Sequence contained an objac of track that was present in the obligonic leotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonalide poly A tail. The sequence tag present in the cDNA between the NotI site and the obligo-dT track served to verify it as a clone from the contained by the sequence tag present in the cDNA between the notI site and the obligo-dT track served to verify it as a clone from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus morvegious
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451 Eckstein Medical Research Building Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
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                                                                                                                                                                                                                                                      Seq primer: Ml3 Forward.
                                                                                                                                                                                                                                                                             Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                          Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                       normalized Eye library cDNA Library Preparation: M.B. Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 319 335 8250
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                                                       /organism="Rattus norvegicus"
/strain="Sprague:Jawley"
/db_xre1="taxon:10116"
/clone="UI-R-Y0-vc-e-12-0-HI"
/clone_lib="UI-R-Y0"
/dev_stage="adult"
/lab_host="DH10B (life Technologies)"
                                                                                                                                                                                                                         Location/Qualitiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1091 taaaaggggqqaaatggaaagggtgetteeaeytgeeeegagetetqtqgetetqtqeqq 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCATGAGIACGGCGAATGGTITGGCTACCIGAACCAAGAGGGAAAAGGTGGCCCTTACCA 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            me44h06.rl Soares mouse panwels,5 Mus musculus chNA clone imAGE:351419 5' similar to PIR:JXO187 JX0187 remin-binding protein
                                                                              Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,L. Geisel,S., Kucaba,I., Lacy,M., J.e,M., Martin,J., Morris,M., Schellenherq,K., Steptoe,M., Tan,F., Underwood,K., Morre,H., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,K. and Waterston,R.
                                                                                                                                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
1 (bases 1 to 349)
                                                                                                                                                                                                                                                                                                                                     Mus musculus
Contact: Marra M/Mouse EST Project
                               Unpublishad (1996)
                                                        The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                             W41312.1 GI:1324602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hybridization with the normalized whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amplified cDNA inserts from previous library clones from which 3' ESIs had been derived were used as a driver in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of origin of a clone within the mixture. The subtracted library (UI-R-Y0) was constructed as follows: PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library. The driver for the subtraction consisted of a pool of all previous libraries (ULR-AO, ULR-AL, HER-EO, ULL-R-ED, and ULL-R-CD). The tay is a string of 3-5 nucleotides present between the Not I site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /more-"vector: pT713)-Pac (Pharmacia) with a modified polylinker: Site_1: Not I: Site_2: Eco RI: The HI R-YU library is a subtracted library derived from an individually lagged normalized whole-eye (minus the lens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligo-dT track which allows identification of the library
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Carnine i.E., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akabira,S., Akiyama,J., Fokoda,S., Pokunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Koylina,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
                                                                                                                                                                                                                                          Enkaryota; Metacoa; Chordata; Ganiata; Vertebrata; Enteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Sources and M.Fatima Bonaldo. kNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."
a 101 e 91 q 79 t
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Hest Local Similarity 65.3%;
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Carnine (F. Shiba'a, K. Osawa, Y. Konno, H. Itoh, M. Aizawa, K. Akabiha, S. Akiyama, L. Fukuda, S. Fukunishi, Y. Funayama, L. Hata Akabiha, S. Konno, H. Itoh, M. Itawa, M. Kawai, J. Itoh, M. Itawa, M. Kawai, J. Kikuchi, M. Kojima, Y. Matsuyama, L. Niitsuma, H., oda, H., owa, C., Sato, K., Shibata, Y., Shiqemoto, Y., Shiraki, T. Soqabe, Y., Soqabara, Y., Sazuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominayan, N., Watanabe, S., Yasume, M., Yamamora, T., Yokofa, T., Yoshino, M., Muramorsu, M., okazaki, Y., and Hayashizaki, Y.
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Thermostabilization and thermosetivation of thermolabile enzymes by trebalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
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Please visit our web site (http://denome.rtc.riken.go.jp) for
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Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
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Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                    Unpublished (1999)
Contact: Chie owa
                                                                                                                                                                                                                                                           ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N. Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
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/clone-"3010001K20"
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                           BACKWARD: GTITICCCAGTCACGACG
Plate: 7 row: J column: 9
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Single pass sequencing. Bases called and trimmed with phred
v0.980904.c. Vector identified by cross_match with the mins
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Thermostabilization and thermoactivation of thermodabile enzymes by
trehalose and its application for the synthesis of full length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the sequence tag present in the cDNA between the NoII site and the olique of track served to identify it as a clone from the normalized adult 12 bay Embryo library, cDNA Library Preparations M. Estima Bonaldo, Ph.D. Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soires, MB
Frogram for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: Ml* Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Research denetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: msoares blue.weeq.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 419 435 9565
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Mammalia; Eutheria; Rodentia; Schurognathi; Muridae; Murinae;
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18: Conservative
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: 419-435-8250
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/db xret "taxon:9914"
/elone lib "MARC 4BoV"
/tissue type-"pooled"
/lab hast-"DH10R"
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/clone "UL R-C2p 14 d 06:0:UL"
/clone lib "UL R-C2p"
                                                                                                                          /strain "sprague bawley
/db xret "taxon:10116"
                                                                                                                                                                                                                         /organism "Rattus norvegieus"
/str.cir "Spraano bawley"
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Rest Local Similarity 66.7%;
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      into DH108 bacteria (Lite Technologies) to generate the ULLR C2p Library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 791 806, 1996)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       believen the Not I site and the oligo dI track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UN R C2P) was constructed as follows: PCK amplified cHNA inserts from ULR C1 clones from which 3 ESIs had been derived was used as a driver in a hybridization with the ULR C1 clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library in the form of single stranded circles. The remaining single stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev.stage="adult"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/hote "Vector: pF7FB Pac (Pbarmacia) with a modified polylinker: Site 1: Not 1: Site 2: Eco RE: The UL R C2p library is a subtracted library derived from the UL R C3 library, which is a subtracted library derived from the UL R C0 library consisted of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constructed from rat placenta, adult lund, brain, liver
kidney, heart, spleen, ovary, muscle, 8, 12 and 18 day
cubryo. The tag is a string of 3.5 nucleotides present
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BASE COUNT

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                   1: /SIDSE/gcqdata/geneseq/geneseqn/NA1980.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No.	Score	Match	Match Length DB		ID	Description
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۸	33.6	2.3	2214	12	Q13580	A.altocetigenes me
ىد	33.5	2.9	2214	_	020383	ADH complex struct
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Haemophilus inflac	Polynucleotide seq	V. marinus PKS lik	Polycystic kidney	Human PKD1 cDNA.		Polycystic kidney		Polycystic kidney	Polycystic kidney	Calcium independen	Nucleotide sequenc	Nucleotide sequenc	M. tuberculosis re	M. tuberculosis an	Mycobacterium spec	Mycobacterium spec	Buman MITHL relate	Arabidopsis thalia	Human G protein co	Human G protein co	Nucleutide sequenc	Stealth virus nucl	Stealth vitus nucl	Human PrAk-doita o	Steroid bormone re	Peroxisome prolite	cDNA encoding rat	A4 amyloid procurs	Human macrophage r	Human marcosk cbNA	Human marcosk clona	EST clone HX50. H

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                              Maru I, Ohta Y, Tsukada Y;
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Query Match Best Local Similarity

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                                                                                                                                                                                                                                                             a membrane bound ADH complex with a 44kb sub unit (cytocho-whose coding sequence is located immediately downstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mixture was used to transform E.coli JM109. Probes were designed based on the N terminal amino acid sequence of the ADH complex isolated from A. alloaceliques (see 01882-01884). The gene
                                                                                                                                                                               whose coding sequence is located immediately encoding the 72kD subjunit. See also 91381.
                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding the 72kD ADH subunit was isolated and sequenced. It forms
         Sequence 2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 20-22 and Fig 3; 36pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alcohol dehydrogenase; acetic acid; termentation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH complex structural gene (72.000 mol. wt. protein)
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                                                                                                                                                                                     872 tüütetaeetgaaeultageaaegattegeeutgaaaetaeaaataeegtteegaaggea 931
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                                                                                                                                                                                                                  707 tyctcaacceangacacygcattgaagccatgtggttcatgatggacattgcccaacyct 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 872 tygtotacetyygcyttggcaacggttegccytggaactacaagtaccyttecgaaggca 931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyctcaacccayyacacygcattyaagccatytyyttcatgatyyacattycccaacyct 766
                                                                                                                    congruent encrantitarian and encountered the encountered encounter
                                                          aggycyacaacctqttcctgggcagcatcytcgcactgaagccggaaaccqurgaatacg
                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                            0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                   Score 33.6; DF
Pred. No. 0.9;
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                                                                                                                                                                                                                                                                                                                                                                             DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                      Length 2214;
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                                                                                                                                                                                                                                  Query Match 2.9%;
Hest Local Similarity 45.7%;
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                       analysis of various overlapping protocadherin cDNA clones revealed that some clones contd. unique sequences at the 3' end. The sequences forming the boundaries of the 3' end regions are
                                                                                                                                                                                                                                                                                                                                                                                                                          contained the putative entire coding sequences of two novel proteins designated protocodherin-4; proteins designated protocodherin-4; (pc42). The DNA and deduced AA sequences of pc42 are in 068997/R58906, while those of pc43 are in 068998/R58907. Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Two tull length human cDNAs corresp. to the partial cDNAs of HUMAN-42 and HUMAN-43 (968981,968982) were isolated trom human letal brain cDNA library. Several overlapping cDNA clones were isolated with each probe including two cDNAs which
                                                                                                                                                                                                                                                                sequences of two possible products of alternative splicing of pe43 mRNA are respectively presented in Q69000/R58912 and Q69001/R49144
                                                                                                                                                                                                                                                                                                                                    consistent with the consensus sequence of {\tt mRNA} splicing, suggesting that these clones may corresp. to alternatively spliced {\tt mRNAs} .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUL-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q69001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q69001 standard; cDNA; 2751 BP
                                                                                                                                                                                                                                 Sequence 2751 BP; 698 A; 715 C; 696 G; 642 T; 0 other;
                                                                                                                                                                                                                                                                                                    The DNA and AA sequences of one possible product of alternative splicing of pc42 mRNA are given in Q68999/R58911. The DNA and AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WP1; 1994-293849/36.
P-PSDB; R49144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09414960-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cadherin; protocadherin; cell adhesion molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Product of alternative splicing of human protocadherin 43 mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 99-102; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for modulating natural binding and regulating activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide sequences encoding new proto:cadherins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DOHE-) DOHENY EYE INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1993;
974 accgrqccqqcqtqcqqcaactattcqccttagaccttqtaaccqqqqatqctqacaatca
                              362 tegeogecatggeetttagteaatatgeettageeagtggggegeaggaagetaaageea
                                                                    914 ttgcaacqgatctggatgaaggccccaacggtgaaattatttactccttcggcaqccaca
                                                                                                         302 tigettiggateaggaaggeaaaceeetgegteaaeeetataaegtiitiiieegaiiget 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (tirst entry)
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115-2160
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                                                                                                                                         Score 33.6; Di
Pred. No. 1;
0; Mismatches
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                                                                                                                                                                            DB 15; Length 2751;
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                                                       these sequences are involved in cell cell adhesion. The proteins may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against the encoded sequences are useful
                                                                                                                                                  cytoplasmic domain of cadherin interacts with the cytoskeleton through
categories and other cytoskeleton associated proteins. The cytoplasmic
domain is not present in all cadherins, but in those which possess it,
                                                                                                                                                                                                                                                                                                                                                                                                             method from those with a cytoplasmic domain. The pathese sequences are involved in cell cell adhesion.
                                                                                                                 not possess a cytoplasmic domain appear to function via a different
                                                                                                                                                                                                 These sequences were isolated after screening a human toetal brain cDNA library (contained within lambdaZapli vectors), with 42p labelled versions of the sequences represented by T03605 and T04665. The abundant spliced version of pc4Z is represented in T03622. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.X
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                                          tor modulating the binding activity
                                                                                                                                                                                                                                                                                                                                          Polynucleotide(s) encoding human protocadherins ped and ped and rat
peb—involved in cell cell adhesion and regulation activities
                                                                                                                                                                                                                                                                                                                                                                                            P PSDB; R87154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Profoscadherin; pe3; pe4; pe5; human; rat; cadherin; ceil adhesion; monse; catenin; therapy; clone; troq; truit tly; ss.
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                                                                                                                                     is essential for the eadherins adhesive function. The eadherins which
                                                                                                                                                                                                                                                               the cDNA close of the human profocadherin sequence, designated pc43.
                                                                                                                                                                                                                                                                            T03624 and T03625 represent possible alternatively spliced versions of
                                                                                                                                                                                                                                                                                                             Example 4; Page 107 110; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANSHOT ( SHOED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 JUN 1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo saptens
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11 | 1 | 11 | 111111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spliced pc43 coding sequence #2.
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L15..2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product - protocadherin clone
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                                          of protocadherins,
                                                                                                    The proteins encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ح</u>
                                          and can be used
                                                          are useful
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Sequence 2751 BP; 698

A: 715 C; 696 G; 642 T; 0 other;

Q68997/R58906, while those of pc43 are in Q68998/R58907. Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       onery Match 2.9%;
Best Local Similarity 45.7%;
Matches 117; Conservative
     contained the putative entire ending sequences of two movel proteins designated protocadhetin-42 (pc42) and protocadherin (pc43). The DNA and deduced AA sequences of pc42 are in
                                                                        Two full length human cDNAs corresp. to the partial cDNAs HUMAN 42 and HUMAN 44 (268981,268982) were isolated
                                                                                                                                                                                        WPI; 1994-293849/36
P-PSDB; R58912.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clones were isolated with each probe including two conas which
                                                          from human fetal brain cDNA library. Several overlapping cDNA
                                                                                                                                              for modulating natural binding and regulating activities
                                                                                                                                                          Polynucleotide sequences encoding new proto:cadherins
                                                                                                                                                                                                                                 Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cadherin; protocadherin; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 44
                                                                                                                  Example: Page 94:96; [14pp; English.
                                                                                                                                                                                                                                                           (DOHE ) DOHENY
                                                                                                                                                                                                                                                                                      29 - DEC: 1992;
                                                                                                                                                                                                                                                                                                                 23 - DEC - 1993;
                                                                                                                                                                                                                                                                                                                                           07 · JUL · 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Product of alternative splicing of human protocadherin 44 mkNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analysis of various overlapping protocadherin cDNA clones revealed that some clones could, unique sequences at the 3' end. The sequences forming the boundaries of the 3' end regions are
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                            WP1; 1996-068874/07.
                                                                                 Suzuki S;
                                                                                                                                 (LOHE: ) DOHENY EYE INST
                                                                                                                                                                                         27 - JUN-1444;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protocadherin: pc4; pc4; pc5; human: rat; cadherin; cell adhesion; catenin; therapy; clone; troq; truit fly; ss.
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45.7%;
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Hest Local Similarity 45.7
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catenins and other cytoskeleton associated proteins. The cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. The proteins encoded by these sequences are involved in cell-cell adhesion. The proteins may have resultatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against the encoded sequences are useful for modulating the bluding activity of protocadherins, and can be used the expectation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           versions of the sequences represented by 103605 and 134606. The abundant spliced version of pc42 is represented in 103622. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         These sequences were isolated after screening a human foetal brain cDNA library (contained within lambdaZapl1 vectors), with 32P labelled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T03624 and T03625 represent possible alternatively spliced versions of the cDNA clone of the human protocadherin sequence, designated pc4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide(s) encoding human protocadherins pes and pes and rat pc5 - involved in cell cell adhesion and regulation activities
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2789 BP; 615 A; 781 C; 761 G; 632 T; 0 other;
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                                                                                            974 accordecydryfgegyraantattryrettaganettyfaaregggafycfgaraatra
                                                                                                                     914 ttqcaacyuatctqqatqaaqqccccaacqqtqaaattatttactccttcqucaqccaca 973
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Q68998 standard; cDNA; 4705
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                                                                                                                                                                                                                    RESULT
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Best Local Similarity 45.7%;
Protocodherin: pes: pes: pes: human: rat: cadherin: cell adhesion: monse; catemin: therapy: clone: trou; fruit fly: ss.
                                                        Protocadherin clone 43 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 typical cadherins but they do have distinct features, both lack the prosequences that are present in all known eatherin precursors. The extracelinlar domains of ped2 and ped3 are different in length and ped2 contains seven subdomains that closely resemble the typical cadherin extracellular subdomain while ped3 has six such domains, the sequences do not show any significant homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (pc43). The DNA and deduced AA sequences of pc42 are in 068997/R58906, while those of pc43 are in 068998/R58907. The overall structures of pc42 and pc43 are similar to that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W| ' | ;
                                                                                                SECTION 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contained the putative entire coding sequences of two novel professions designated profocadherin 43 (pc42) and profocadherin 43
                                                                                                                                          TH 45.121
                                                                                                                                                                            103622 standard; cDNA; 4705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from human fetal brain cDNA library. Several overlapping cDNA
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pc5—involved in cell-cell adhesion and regulation activities
1154 acaacgeeecqqaqat 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to
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P PSDB: R87147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the protein may have regulatory functions in the cell, as well as the cell cell adhesive properties. Antibodies produced against the encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function via a different method from those with a cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytoskeleton through catenins and other cytoskeleton associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence, designated pc43. This sequence was isolated after screening human toetal brain cDNA library (contained within lambdaZapil vectors).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3: Page 79-84; 146pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The protein encoded by this sequence is involved in cell cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The cytoplasmic domain is not present in all cadherins, but in those
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with 32P labelled versions of the sequences represented by
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                                                             542 aceterieetiquagat 557
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45.7%;
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Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a human growth factor designated zapol. Zapol is an andiopoletin homologue. The polypeptide is used to stimulate cell growth and tissue development. The polypeptides form multimeric proteins. Zapol has angiogenic or hematopoletic activity. Zapol the proteins can be used in assays for anglogenic activity. Zapol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue development; multimeric protein; hematopoietic; angiogenic; tissue revascularization; full-thickness skin wound; venous stasis ulcer; tracture repair; skin grafting; reconstructive surgery;
                                                                                                                                                                                                                                                                                                                                                                                                                                  surgery, and establishment of vascular networks in transplanted cells and tissues. Zapol is also useful as a research agent, such as in the expansion of hematopoietic cells (including stem cells) and endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins may be used therapeutically to stimulate revascularization of tissue. Specific applications include treatment of full-thickness skin wounds, including venous stasis ulcers and other chronic, non-healing wounds, as well as fracture repair, skin grafting, reconstructive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zapo), a novel andiopoietin nemocogae, and for developing the study and regulation of angiogenesis and for developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 54; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conklin DC. Presnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; growth factor; zapol; angiopoletin homologue; cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Degenerate DNA encoding a human growth factor designated capol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X85600 standard: DNA; 1218
                                                                                                                                                                                                                                                                                                                                                               Sequence.
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                                     tnyaraarytnoaywsnathatgggngaymynaaywsnmgnytngcngtncarytnmgng 835
                                                                        tityaayuunytiyeteaaeeeaggaeaeyueattyaayeeatyiyutteatyatygae 753
                                                                                                             danceadaaaladgattaatgegggaagegdtdanneeadadadadatttyttgatagt 693
                                                                                                                                                                                  cnwsndayddnddntddacndthathearmdnmdneaydayddnwsndthdayttyaaym 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a novel andiopoletin homologue, and related DNA, useful for
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RESULT 11
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Best Local Similarity 49.4%;
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                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes a human GPPase-activating protein (196API). The protein has an "IO motif" which is defined as an amino acid sequence of 20-40 amino acids in length containing an isolencine residue immediately collowed by a glutamine residue which has at least 50 percent sequence similarity to the consensus sequence shown in W18823. The DNA sequence used for production of recombinant 196API, which is useful in the diagnosis and treatment of tumonrs characterised by aborrant ras
                                                                                                                                                                                                                                                                                                                  expression. Detection of mutations in the 196AP1 gene is diagnostic of cancer. The 196AP1 protein can be used for treatment of cancer to reduce the activity of p21-ras. Detection of neoplastic cells can be achieved by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding GIPase-activating protein LyGAPL - for producing recombinant protein useful for tumour diagnosis and therapy
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tumour: suppressor: ras: cancer; p21-ras; neoplastic cell; ds.
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                                                                                                                                                                                                                                                                    Sequence 7573 BP; 2320 A; 1570 C; 1680 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Column 21-28; 35pp; English.
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                                                                                                                 1872 ATTCCAATGCCCTGTTGATCAGGGCCACCGATGACAACATCTCCACTGCGACAGAGAGCT 181
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              972 agaaaaatgttggcaafggtttgagcgggtccafgattacgcctggagfcaf
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Location/Qualifiers
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                                                                                                                                                                                  0: Mismatches
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                                                                                                                                                                                              Score 32.8; Ti
Pred. No. 3.4;
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   VHHHY: /;
                                                        VBBB57 standard; cDNA; 775
                                                                                                                                                                                                                                       Claim 1; Fig 4; 21pp: Japanese
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F PSDB; R15470;
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Oberty Match 2.7%; Score (2.2; D8-20; Best Local Similarity 49.1%; Pred, No. 1.4;
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harmatopolesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; ESI; human; chemotaxis; chemokinesis; harmastaxis; gene therapy; thrombalysis; receptor; ligand; anti inflammatory; tumour inhibitor; ds.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             forms of HMurroSR which may be associated with a dysfunction and can define a diagnosis of a disease (or susceptibility to a disease) resulting from altered HMarcoSR expression.
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treating e.g. cardiovascular disorders, septic chock, bacterial
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define a diagnosis of a disease (or susceptibility to a disease)
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tailure, endotoxaemia and intections caused by gram negative and
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Search completed: January 1, 2001, 22:23:45 Job time: 12006 see

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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
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Perfect score:
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| atgattqrrcatcgccgtca.....rtctccaacttrcygttagt 1173
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Gepyriaht (c) 1993 - 2000 Compuden Ltd
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/cyn2_6/ptodata/2/ina/5D_COMH.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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NO.	Score	Mat ch	Length	DΒ	ID	Description
:	134.2	11.4	1209	2	US-08-553-703A-5	Sequence 5, Appli
2	134.2	11.4	1209	2	8-553-7U3A-	9
بد	134.2	4	1209	4	-09	уī
4	134.2	11.4	1209	4	-006	Ġ,
ហ	33.6	2.9	2214		US-07-985-458-1	1,
5.	34.6	2.9	2751	_	US-07-998-003A-106	106
7	33.6	2.4	2751	_	US-08-453-274H-106	106,
Œ	33. 6	2.3	2751	2	901-858-69-80-80	- - - - - - - - - - - - - - - - - - -
ĵ.	34.6	2.3	2751	N	US-08-268-161A-106	106,
10	33.6	2.9	2751	نيا	US-08-453-702A-106	106,
11	33.6	2.9	2751	6	PCT-US93-12588-106	106,
12	33.6	2.9	2751	5	PCT-US95-08071-106	Sequence 106, App
- 3	33.6	2.5	2789		US-07-998-003A-104	Sequence 104, App
- 4	33.6	2.4	2789	_	US-08-453-274H-104	104
5	33.6	2.4	2789	Ν.	US-08-453-695A-104	Sequence 104, App
16	33.6	2.4	2789	2	US-08-268-161A-104	104,
17	بد د د	2.9	2789	ند	US-08-453-702A-104	Sequence 104, App
18	33.6	2.9	2789	9	PCT-US93-12588-104	104,
1 '4	33.6	2.9	2789	6	PCT-US95-08071-104	104,
20	33.6	2.4	4705	_	US-07-998-003A-96	96, 1
21	33.6	2.4	4705	_	US-08-453-274B-96	96,
2.2	33.6	2.9	4705	2	US-08-453-695A-96	96,
23	33.6	2.9	4705	٧.	US-08-268-161A-96	96,
24	33.6	2.9	4705	ىب	US-08-453-702A-96	Sequence 96, Appl
2,7	33.6	2.4	4705	6	PCT-US93-12588-96	Sequence 96, Appl
26	44.6	2.9	4705	\$	PCT-US95-08071 96	96,

Sequence 126, A	US-08-127-954-126	76 1	2	2.4	28.4	4	
Sequence 113, A	US-08-127-954-113	76 1	2	2.4	28.4	44	
Sequence 112, A	US-08-127-954-112	76 1	276	2.4	28.4	4 3	
Sequence 17, Ap	US-09-128-155-15	73 5	17637	2.5	29.4	42	
Sequence 3, App	US-08-360-673-3	03 1	25	2.5	29.6	4 1	
Sequence 40. Ap	US-08-149-223A-40	01 5	17	2.5	29.6	40	0
Sequence 40, Ap	US-08-458-731-40	01 5	1.7	2.5	29.6	5	C
Sequence 40, Ap	US-08-480-150A-40	01 4	17	2.5	29.6	8	C
Sequence 40, Appl	US:08-484-596A-40	01 4	17	2.5	29.6	3.7	0
Sефиенсе 40, Ар	US-08-484-158B-40	01 4	17	2.5	29.6	36	3
Sequence 40, App	US-08-484-993B-40	01 3	17	2.5	29.6	ن <u>د</u> ئ	Э
4-	US-08-658-136-4	60 5	140	2.6	30	4	C
Sequence 1. App	US-08-460-751-1	12 3	129	2.6	3 ⊂	ابد ابد	C
Sequence 1. Appl	US-08-680-897-1	80 5	96	2.5	30.6	7.	ာ
Sequence 2, App.	US-08-759-444-2	78 2	88	2.6	30.6	Ξ	3
Sequence 5, Appl	US - 08 - 483 - 488 - 5	04 3	38	2.7	3.2	3.0	
Sequence 1, Appl	US-08-794-795-1	03 4	1703	2.7	32.2	29	
Sequence 5, Appl	US-08-794-795-5	60	15	2.7	32.2	28	
Sequence Z. Appl	7 6.6 707.00.50					ŧ	-

ALIGNMENTS

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; Sequence 5, Application US/08553703A ; Patent No. 5795767
US - 08 - 553 - 703A - 5
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                                                                                                                                        INFORMATION FOR SECTIONS: 5:
                TOPOLOGY: Tinear MOLECULE TYPE: CDNA
                                                                                                                                                                                                 REFERENCE/DXXKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 30-N/V-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MAKU, ISAFUMI
APPLICANT: GHIA, YASUHIRO
APPLICANT: ISUKADA, YOJI
TITLE OF INVENTION: EPIMERASE
NUMBER OF SEQUENCES: 9
                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   FILING DATE: AUTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DAIA
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                                                    LENGTH: 1209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                            NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM LYPE:
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                                                                                                                                                                              TELEPAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/553,703A
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Query Match II.4%: Score 134.2: DB 2: Lebath 1209; Best Local Similarity 48.3%; Pred. No. 1c 44;

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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 34,115
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GENERAL INFORMALION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72 mb
                                        FILING DATE: 26-MAR-1990 AITORNEY/AGENT INFORMATION:
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1991
FILING DATE: 20 FEB-1991
APPLICATION NUMBER: 73440/1990
                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                            COMPUTER: HAM PC compatible (NEC PC-9801 ES)
OPERATING SYSTEM: MS DOS
SOFTWARE: ASCIT FORM
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
REGISTRALION NUMBER:
                        NAME
                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/985,458
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                      Goodman, Herbert
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Fukaya, Masahiro;
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Alcohol Dehydrogenase Complex, Plasmid
Containing The Same And Transformed Acetic Acid
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                                                                                                                                                                                                                                                                   Sequence 106, Application US/07998003A Patent No. 5643781
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                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                            APPLICANT: Suzuki, Shintaro
THILE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 107
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                 COUNTRY:
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STRANDEDNESS: double
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-100S/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 972-1400
TELEFAX: (212) 870-1622
                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Morray, ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL.:
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                                                                                                                                 STREET:
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                                                                   60603
                                                                                                                 Chicago
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Cloning and Sequencing of the Gene Cluster
Encoding Two Subunits of Membrane-Bound
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                                                                                                                                 20 South Clark Street
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                                                                                  USA
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Fukaya, Masahiro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochimica et Biophysica Acta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nishiyama, Makoto;
Horinouchi, Sucharu and
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53.9%; Pred. No. 0.4;
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US 08 454 274B 106
; Sequence 106, Application US/08453274B
; Patent No. 5663300
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                   CURRENT APPLICATION DATA:
                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: $12/346-5750
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                                                                                                                                                                                                                                                                                                      APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1104 ACAACGCCCCGGAGAT 1169
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                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       NUMBER OF SECHENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1094 AGGGGGCAATGCCGAAGGGAGCACATTGCAAAGTGTTGGTGGAGGTTGTGGATGTGAATG 1153
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                                                       MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC DOSZMS-DOS
                                                                                                  STATE WILL GIM
                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                      CITY: Chicago
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SIRANDEDNESS: single
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                                        SOPTWARE:
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  ADMILITATION NUMBER
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                                                                                                                                             6,05,06, 6,4,02
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16300 Sears Tower, 233 South Wacker Drive
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US/08/453, 274H
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: Patent No. 5708143
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Best Local Similarity 45.7%;
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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ATTORNEY ASENT INFORMATION:
NAME: No. 566 $400 and, Greta E.
REGISTRATION NUMBER: 35, 302
REFERENCE/DOCKET NUMBER: 32660
ALTORNEY/AGENT INFORMATION
                                                              APPLICATION NUMBER: US
                                                                                                                                                                                              COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Protocadherin Materials and Methods NUMBER OF SEQUENCES: 115
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                                                                                                       MEDIUM IYPE: Floppy disk
COMPULER: IBM Fe compatible
OPERALING SYSTEM: PO DOSAMS DOS
SOFIWARE: Patentin Release #1.0, Version #1.25
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                      CLASSIFICATION:
                                            FILING DATE:
                                                                                                                                                                                                                       2 I P :
                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                             STALE:
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LOCATION: 115...2160
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nucleic acid
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Pred, No. 0.45;
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INFORMATION FOR SEQ ID NO: 106:
                                                                                                           COMPUTER READABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: ITM PT COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 2751 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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REFERENCE/DOCKEL NUMBER: 32658
LELEDOMMUNICALL N. INFORMATION:
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                                   ATTORNEY/AGENT INFORMATION:
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                                                     CLASSIFICATION:
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LOCALION: 115...2160
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REGISTRATION NUMBER: P-41,337
                    NAME:
                                                                                                APPLICATION NUMBER:
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                                                                            June 27, 1994
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US-08-453-702A-106
; Sequence 106, Application US/08453702A
; Patent No. 5891706
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                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IFROOD TIBLE
OPERALING SYSTEM: PG-DOS/MS-DOS
SOFTWARE: Parontin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       ALE.: 25
STREET: 25
CHY: Chicago
CHY: Illinois
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Meri
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                                                           ATTORNEY/AGENT INFORMATION:
NAME: No. 5891706and, Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
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LOCATION: 115..2160
                                                                                                      CLASSIFICATION: 435
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STRANDEDNESS: single
                                                                                                                               FILING DATE
                                                                                                                                                 APPLICATION NUMBER: US/08/453,702A
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                    REFERENCE/DOCKET NUMBER:
                               NAME: No. 5891706and, Greta
REGISTRATION NUMBER: 35,302
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                                                             Greta E.
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PCT US93 1258B 106
Sequence 106, Application PC/TUS931258B
GENERAL INFORMATION:
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Rest Local Similarity 45.7%;
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                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IRM PC compatible
OPERALING SYSIEM: PC-DOS/MS-DOS
SOFIWARE: Patentin Release #1.0, Version #1.25
                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THTLE OF INVENTION: Protocadherin Materials and Methods NUMBER OF SEQUENCES: 107
TELLECOMMUNICATION INFORMATION:
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LENGTH: 2751 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1094 AGGCCGCCAATCCCGAAGGACCACATTGCAAAGTGTTGGTGGAAGGTTGTGGATGTGAATG 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T034 AGGEFOGGETGGACT FCGAGGACACCAAACTCCATGAGATETTACATCCAGGCCAAAGACA T093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    482 agaagteetateeaggtaetagaeeeeteaaateeetggeggtgeegatgattitageea 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422 Etyceetyeagyeetaeaataaegteetaegeegteageacaateeeaaaggteaataeg 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  802 THYCLTHIGGALCAGGAAGGCAAAGCCCCLACGCCCCALAAGCGLLLLLLLCCGALLACC 361
                                  NAME: Noland, Greta E
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        862 tenjeciatiyacetitagteaatatgeettageeaytiyyggegeaggaagetaaageea 421
                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
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LOCATION: 115...2160
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              REFERENCE/DOTKET NUMBER:
                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: purioic acid
STRANDEDNESS: single
                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Marray, & ADDRESSEE: Borun
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                0; Mismatches 139; Indels
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; LOCATION: 115
PCT 1893-12588-106
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GENERAL INFORMATION:
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Best Local Similarity 45.7%;
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                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1154 ACAACGCCCCGGAGAT 1169
                    ATTORNEY/AGENT INFORMATION:
                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Protocadherin Materials and Methods
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                                                                                                FILING DATE:
                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERALING SYSTEM: PC DOS/MS DOS
                                                                                                                                                                                                                                                                                                                                                                                   SIREET: 6300 S
                                      APPLICATION NUMBER: US 07/998,003 FILING DATE: 29 DEC 1992
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/08071
                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                       STAIR:
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, ADDRESSEE: Borun
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Notand, Greta E.
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Pred. No. 0.45;
0; Mismatches 189; Indels
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INFORMATION FOR SEQ ID NO: 106:
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REFERENTE/OFFKET NUMBER: 32
LETETHMMINICALION (NEGMATION:
LELEPHONE: 3:2/474-6300
                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LENGTH: 2751 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                              CLASSIFICATION: 435
AFFORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILLE OF INVENTION: Protocadherin Materials and Methods NUMBER OF SEQUENCES: 107
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                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTEK: THM PC compatible
OPERALING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 115..2160
                                                                                                            APPLICATION NUMBER: FILING DATE:
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                       REGISTRATION NUMBER:
                                              NAME:
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REFERENCE/DOCKET NUMBER:
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                  No. 5643781and, Greta E. RATION NUMBER: 35,302
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APPLICANT: Suzuki
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                 STREET: Chicago
CITY: Chicago
TMATE: Illinois
Unnited
                                                                                                                                                                 CURRENT APPLICATION DATA: US.
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LENGTH: 2789 base pairs
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                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1034 AGGGTCGGGTTCGAGGACACCAAACTCCATGAGATTTACATCCAGGCCAAAGACA 1094
                               TELECOMMUNICATION INFORMATION: 312/474-6300
                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1094 AGGGCGCCANTCCCGNAGGAGCACATTGCANAGTGTTGGTGGAGGTTGTGGATGTGANTG 115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 togoogocatggootttagtoaatatgoottagooagtgggggggaggaagotaaagooa 42]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 ttgetttggateaggaaggeaaaceeetgegteaaceetataaegttttttteegattget 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 2.9%; Score 44.6; DB
Local Similarity 45.7%; Pred. No. 0.45;
                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LECOMMON. 3127 ...
TELEPHONE: 3127 ...
TOPAX: 312/984-9740
                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 115
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                                                                       REFERENCE/DOCKET NUMBER:
                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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TELEX:
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                                                                                                     No. 5663300and,
25 - 3856
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6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki, Shintaro
                 312/474-0448
                                                                                                                                                                                                  Patentin Release #1.0, Version #1.25
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107
                                                                                                                                                                 US/08/453,274B
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                                                                                                           Greta E.
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIFLE OF INVENTION: Protocadherin Materials and Methods NUMBER OF SEQUENCES: 115
                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: $12/474 -6300
                                                                                                                                                                                                                                                                                                                         NAME: NO. $708143and, Greta E.
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comPUTEK: IBM PC compatible
chekAFING SYSTEM: PC DOSYMS-DOS
SPETWARE: Putent ID Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                           TELEX:
                                                                                                                  TELEFAX:
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FYPE: meloic acid

STRANGENESS: single
                                                                                                                                                                                                                                                  REFERENCE/LOCKET NUMBER:
                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/453,695A
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LOCATION: 115...2622
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Best Local Similarity 45.7%;
Matches 117; Conservative
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1154 ACAACGCCCCGGAGAT 1169
                                                                   1094 AGGGCGCCAATCCCGAAGGAGCACATTGCAAAGTGTTGGTGGAGGTTGTGGATGTGAATG 1153
                                                                                                                                         1034 AGGGTCGGCTGGACTTCGAGGACACCCAAACTCCATGAGATTTACATCCAGGCCAAAGACA 109
                                                                                     482 agaagteetateeaggtaetagaeeeeteaaateeetggeggtgeegatgattttageea 54]
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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LOCATION: 115
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Pred. No. 0.45;
0; Mismatches 139; Indels 0
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Search completed: January Job time: 12635 sec 2001, 22:21:59

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Post-processing: Minimum Match 0%
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1 MIAHRRQELAQQYYQALHQD......CFHVPRALMLCAETLQLPVS 391
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SwissProt_39:*
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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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P13685 escherichia	P05803 intluenza a	P21951 saccharomyc	Q59749 rhizobium m	09z8m3 chlamydia p	P38016 chlamydia m	P53008 saccharomyc	Q92178 qallus qall	P15057 bacteriopha	Q39610 chlamydomon	Püss61 dietyoglomu	Ν.	Q29451 bos taurus	P26221 therromonos	P75368 mycoplasma		043280 homo sapien	_	PO4254 panulirus i	-	P27033 pseudomonas	•	P49606 ustilago ma		053175 mycobacteri		046432 felis silve	P37512 bacillus su	_	P29954 rhizobium m	P51606 homo sapien	P51607 rattus norv	P17560 sus scrofa	Description

P20906 pseudomonas	P20906	MDLC_PSEPU		528	3.8 8	82.5	Ú
vibito che	129481	HORIA DOLD.	_	489	3.8	82.5	4
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4 clostridium	P04954	GUND_CLOTM	_	649	3.9	83	99
or yet olago	P19813	TREA_RABIT		578	3.9	83	œ
neurospora	Q01291	RSO_NEUCR	_	293	3.9	83	7
saccharon;	P23466	CYAA_SACKI.	_	1839	3.9	83.5	6
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his SWISS-PROT entry is copyright. It is produced through a cotween the Swiss institute of Bioinformatics and the EMH. he European Bioinformatics institute. There are no restrict se by non-profit institutions as long as its content is soldlied and this statement is not removed. Usage by and to notifies requires a license agreement (See http://www.isb-sib.	-!- PATHWAY: N-ACETYLNEUHAMINIC ACID BIOSYNIHESIS!- SUBHUNIT: HOMODIMER!- TISSUE SPECIFICITY: KIDNEY, LIVER, ADRENAL, AND PHIDHTARY GLANDS -!- THE AMOUNT BEING MUCH GREATER IN KIDNEY THAN IN THE OTHER TISSUES.	HANNOSAMINE: A CATALYTIC AMOUNT OF ATP IS ESSENTIAL FOR THE GLCCNAC 2-EPIMERASE ACTIVITY.	-1- FUNCTION: CATALYZES THE INTERCONVERSION OF N-ACETYLAGUCOSAMINE TO N-ACETYLMANNOSAMINE, BINDS TO RENIN INSEMING A PROTEIN COMPLEX CALLED HIGH MOLECULAR WEIGHT (HWW) RENIN AND INHIBITS RENIN ACCUPATE ACCUPATE ACCUPATE A CONTENT OF ACCUPATE ACCUPATE ACCUPATE ACCUPATE ACCUPATE ACCUPATE ACCUPATE ACCUPATE ACCUPATE ACCURATE ACCUPATE ACCUPATE ACCUPATE ACCUPATE ACCUPATE ACCUPATE ACCURATE ACCUPATE ACCU	TISSUE-KINNEY CORTEX: MEDLINE: 96279179. Maru I., Ohta Y., Murata K., Tsukada Y.; "Molecular cloning and identification of N-acyl-D-glucosamine "Molecular cloning and identification of N-acyl-D-glucosamine 2-epimerase from porcine kidney as a renin-binding protein.": J. Biol. Chem. 271:16294-16299(1996).	MEDLINE; 91268065. Inoue H., Takahashi S., Fukui K., Miyake Y.; "Leucine zipper motif in porcine renin-binding protein (RnBP) and its relationship to the formation of an RnBP-renin heterodimer and an RnHP homodimer."; J. Hiol. Chem. 266:11896-11900(1991). [3] [3] [3] [3] [3] [4]	SEQUENCE FROM N.A., AND SEQUENCE OF 4-12 AND 326-357. **ILSSUE-KIDNEY: MEDITINE; 90216671. **DOUG H., FUKUI K., Fakahashi S., Miyake Y.; **Molecular clouing and sequence analysis of a cDNA encoding a porcine kidney remin-binding protein."; J. Biol. Chem. 265:6556-6561(1990). [2] [LEUCINE-ZIPPEK, AND MUIAGENESIS.	Ol-AUG-1990 (Rel. 15, Created) Ol-AUG-1990 (Rel. 15, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 30-MAY-2000 (Rel. 39, Last annotation update) N-ACYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.8) (GLCNAC 2-EPIMERASE) (N-ACETYL-D-GLUCOSAMINE 2-EPIMERASE) (RENIN-BINDING PROTEIN) (RNBP). REMBP. Sus scrofa (Pig). Sus scrofa (Pig). Sus scrofa (Pig). Sus scrofa (Pig). Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. [1]	

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35.6%; Pred. No.
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Best Local Similarity 34.7
Matches [18]; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inoue H., Takahashi S., Fukui K., Miyake Y.;
"Genetic and molecular properties of human and
proteins with reference to the function of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D10232; BAA01082.1; MIM; 312420; -.
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or send an email to license/isb-sib.ch).
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PATHWAY: N-ACELYLNEURAMINIC ACTO BIOSYNTHESIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER.
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                                     EWFGYLNERGEVILINI.KGGKWKGGFHVPRALWI.GAETI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECEYTMAMNELWRATGEVRYQTEAVEMMDQIVHWVQEDASGLGRPQLQGAPAAEPMAVP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KERETLQAWKERVGQELDRVVAFWMEHSHDQEHGGFFTCLGREGRVYDDLKYVWLQGRQV 62
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                                                                                      DADNECETQLEWAMKLWWPHSEAMIAFLMGYSDSGDPVLLRLFYQVAEYIFRQFRDPEYG
                                                                                                                                                                                                               PGCLGROONPGHILEAGWELLRHCIRKGDPELRAHVIDKFLLLPFHSGWLPDHGGLFYFQ
                                                                                                                                                                                                                                                                       DSFEGRLLNPGHGIEAMWEMMDIAQRSGDRQLQEQAI-AVVLNTLEYAWDEEFGGIFYFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WMYCKLYRIFERFRHAQLLDAAKAGGEFLLRYARVAPPGKKCAFVLTRIORPVKVQRFIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WQFAVFYNRLE--PKPQWLEIARHGADFLARHGR--DQDGNWYFALDQEGKPLRQPYNVF 117
                                                                                                                                                    DROGHTTGOTEMDQKLWWVHLETTLVALAKGHQATGOTKCWQWFTKVHDYAWSHFADTFYG 348
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01-APR-1993 (ROL
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30-MAY-2000 (Rel. 49, Last annotation update)
MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.4.1.8) (PHOSPHOMANNOSE ISOMERASE)
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Baeteria: Proteobaeteria: alpha subdivision:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 122:35-43(1992).
-!- CATALYTIC ACTIVITY: D-MANNOSE 6-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmidt M., Arnold W., Niemann A., Kleickmann A., Puehler "The Rhizobium meliloti pmi gene encodes a new type of pho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PMI) (PHOSPHÖHEXOMUTASE).
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or send an email to license*isb-sib.ch).
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292 DESVADPTARLWPQTEWLKAAIRFAALTEG
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                                                                                                                                                                                             LLPPTTVEEV-----LAQTVREVMTD-FLDPEIGLMRE: ----AVTPTGEFVDSFEG 244
                                                                                                                                                                                                                                    ERGAEMV - - - GRSDKLRRQLEARCKHPLAGFEEDDPPRLPLGS - - - · · · ·
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                                                                                                                                                                                                                                                                                                                                                  WLEIARHGADFLAR-HGRDQDGNWYFAL-DQEGKPLRQPYNVFSDCFAAMAFSQYALASG 134
                                                                                                                                                                                                                                                                                                                                                                                             LNDAALPLWROKGFDGEGGGEVETIDMKGEPTRDDRRSKVOPROVYCFAA-AGKRGWDGD-74
                                      DRQGHPPQQLEWDQKLWWVHLETLVALAKG 318
                                                                         RIVEPOHLEEWAWLLLRWAERRGN----AQAIVKARRLEETGEKDOTOPDRDVVVMTLED
                                                                                                                RLLNPGHGIEAMWFMMDIAORSGDRQLQEQAIAVVLNTLEYAW - - - - - DEEFGGIFYFL
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01 off 1994 (Rel. 30, Created)
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21.1%; Pred. No. 4.4e-05;
vative 63; Mismatches 166
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4.6%; Score 98.5; DB 1; Length 689;
Hest Local Similarity 21.1%; Pred. No. 1.2;
Matches 55; Conservative 47; Mismatches 100; Indels 5
                                                                                               194442.

10 MAY 2000 (Rel. 4), Created)

10 MAY 2000 (Rel. 4), Last sequence update)

10 MAY 2000 (Rel. 4), Last annotation update)

10 MAY-2000 (Rel. 4), Last annotation update)

LYSOSOMAL ALPHA-MANNOSTIASE PRETURSOR (PC 4.2.1.24) (MANNOSTIASE,

ALPHA B) (LYSOSOMAL APID ALPHA MANNOSTDASE) (LAMAN).
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Pelis silvestris calus (Cat).
Eukaryota: Medazoa: Chordata: Cianiata: Vertebrata: Euteboostomi
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SUB11LIST; BG10040; YYAL.
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MEDI INE:
                 SEQUENCE
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or send an email to licensewisb-sib.ch).
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KDA PROTEIN IN TELB-EXOA INTERGENIC KEGION

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hiochem. J. 328:863-870(1997).
-i. FUNCTION: NEVERSARY FOR THE CATABOLISM OF N-LINKED CARBOHYDRATES
RELEASED DURING GLYCOPROTEIN TURNOVER (BY SIMILARITY).
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      01 - NOV - 1997
                                                            P8088;
                                                                                 HCY_PALVU
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-!- DISEASE: DEFECTS IN MANB ARE THE CAUSE OF LYSOSOMAL ALPHA-
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Pred. No. 2.3;
51; Mismatches
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Comp. Biochem. Physiol. 115B:243-246(1996).
-!- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
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Eumalacostraca; Eucarida; Decapoda; Pleocycmata; Palinura;
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                                                                                  VARIANI
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Best Local Similarity

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80 MAY 2000 (Rel. 9) Created)

80 MAY 2000 (Rel. 9) Last sequence update)

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VALYE TRNA SYNTHETASE (FC 6.1.1.9) (VALINE TRNA LIGASE) (VALKS)

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                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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i caralytic activity at t. Valite + Trna(Val.)
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                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restriction
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                                                                                                                                                                                                                                     send an email to license isb sib.ch)
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                                                                                                 11 PROPERTY.
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Matches 74; Conserv
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BLUDING
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PROSITE: PSOUTTS: ARLTHNALLIGASE I: 1.
Ambinoacyl-trna synthetase; Protein blosynthesis; Ligase; AIP binding.

"HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                  000754; 094094; 016680; 015330;
15.JHL-1998 (Rel. 46, Created)
15.JHL-1998 (Rel. 46, Last sequence update)
40.MAY-2000 (Rel. 49, Last annotation update)
1.YSOSOMAL ALPHA MANNOSIDASE PRECURSOR (EC. 3.2.1.24) (MANNOSIDASE, ALPHA H) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN).
MANZHI OR MANH OR LAMAN.
                                                                                                                                                   siblings."
                                                                                                                                                                    mannosidase cDNA and identification of
                                                                                                                                                                                                                                          MEDILINE:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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               (MANH)."
                                                 Riise H.M.F., Berg I.,
Ceccherini I.;
                                                                                    MEDITINE:
                                                                                                                                   Hum. Mot. Genet. 6:717
                                                                                                                                                                                    Hansen G.M., Malm D., Tranebjaerg L., Tollersrad O.K.;
"Alpha-mannosidosis: functional cloning of the lysosomal alpha
                                                                                                                                                                                                                     Nilssen O., Berg T., Riise H.M.F., Ramachandran U., Evjen G.,
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANT LEU
                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MA2B_HUMAN
                             "Genomic structure of the human lysosomal alpha mannesidase deno
                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                         LISSUE LUNG, AND SKIN;
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42:200-207(1997).
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                                                                Nilssen O., Romeo G., Tollersind C.K
                                                                                                                                     726(1997)
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"Cloning, expression, purification, and characterization of the human broad specificity lysosomal acid alpha-mannosidase.";
J. Biol. Chem. 271:28348-28358(1996).
                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensedisb-sib.ch).
                                                                                                                        use by non-profit modified and this st entities requires a
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                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Nebes V.L., Schmidt M.C.;
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                                   EMBL
                                                       EMBI.,
                                                                      EMHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Spectrum of mutations in alpha-mannosidosis."; Am. J. Hum. Genet. 64:77-88(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Missense and nonsense mutations in the Tysosomal alpha-mannosidase gene (MANB) in severe and mild forms of alpha-mannosidosis."; Am. J. Hum. Genet. 63:1015-1024(1998).
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"Partial sequence of the purified
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                                                                                                                                                                                                                                             DISEASE: DEFECTS IN MANB ARE THE CAUSE OF LYSOSOMAL ALPHA-MANNOSIDOSIS (AM), A LYSOSOMAL STORAGE DISEASE CHARACTERIZED BY ACCOMULATION OF UNBRANCHED OLIGOSACCHARIDES CHARACTERIZED BY ACCOMULATION OF UNBRANCHED OLIGOSACCHARIDES CHAINS. THIS ACCOMULATION OREDOMINANTLY IN THE CAS AND PARENCHYMATUOS ORGANS. ACCOMULATION PREDOMINANTLY IN THE CAS AND PARENCHYMATUOS ORGANS. DEPENDING ON THE CLINICAL FINDINGS AT THE AGE OF ONEST. A SEVERINE INFONTILE (TYPE I) FORM OF ALPHA-HORSNILLE (TYPE II) FORM OF ALPHA-MANNOSIDOSIS ARE RECOGNIZED. THERE IS CONSIDERABLE VARIATION IN THE CLINICAL EXPRESSION WITH MENTAL RETARLATION, RECURRENT INCECTIONS, IMPAIRED HEARING AND JURLER-LIKE SKELETAL CHANGES BEING THE MOST CONSISTENT ABNORMALITIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: FIRST PROCESSED INTO 3 PEPTIDES OF 70 KDA, 42 KDA (D) AND 13/15 KDA (E). THE 70 KDA PEPTIDE IS FUNTHER PROCESSED INTO THREE PEPTIDES (A, B AND C). THE A, B AND C PEPTIDES ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NOT
ALPHA-D-MANNOSE RESIDUES IN ALPHA-D-MANNOSIDES
SUBCELLULAR LOCATION: LYSOSOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDES (A, B AND C). THE DISULFIDE-LINKED. PIM: HEAVILY GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: NECESSARY FOR THE CATABOLISM OF N-LINKED CARBOHYDRATES RELEASED DURING GLYCOPROTEIN TURNOVER. CLEAVES ALL KNOWN TYPES O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "tial sequence of the purified profesin confirms the identity of coding for human Tysosomal alpha-mannosidase B."; hem. J. 305:363-366(1995).
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                  U60899;
U60885;
U60886;
                                                                      U60266; AAC34130.1;
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                                                                                                                                             statement is not removed.
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Hydrolase; Glycosidase; Glycoprotein; Lysosome;
Disease mutation; Polymorphism.
                                                  CONFLICT
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E -> "
             1. -> P (IN AM).

/FTId-VAR 003348.

D -> V (IN REF. 1).

MISSING (IN REF. 4).

P -> H (IN REF. 3).
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R -> W (IN AM;
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                                                                                                                                                                                                                                                        /FT1d-VAR_003342
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                                                                                                                                             -> R (IN AM)
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> H (IN REF. 3).
11425F6A340F33E1 CRC64;
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ALPHA-MANNÓSIDASE B
ALPHA-MANNÓSIDASE C
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Best Local Similarity
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                                                      ARHGRDQDGNWYFALDQEGKPLRQPYNVFSDCFAAMAFSQY-ALASGAGEAKATALQAYN
                                                                                     Conservative
                                                                                               17.7%;
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                                                                                                 Score 94.5;
Pred. No. 4
-EKSYPGTRPLKSLAVPMILANLT - - - -
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01 FEB 1996 (Rel. 43, Last sequence update)
01 of 1996 (Rel. 44, Last annotation update)
ALENYLATE CYCLASE (FC 4.6.1.1) (ATF PYROPHOSPHAFE-LYASE) (ADENYLYL CYCLASE).
                                                           NIVWEL
                                                                                                                                                                                                                                                                                                                                                                                                       Genes 1697. 8:2805-2815(1994).

FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryotas Pundis Bas
Ostiladinomycetidaes
                                                                          Lyases
                                                                                         PHAM; PHOOSED; LER; IS
                                                                                                                                                                                                   entities requires a license agreement (see http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                              This SWISS PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Ricinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gold S., Duncan G., Barrett K., Kronstad J.W.;
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                                                                                                                       INTERPROS IPROOFSEL;
                                                                                                                                                                                     or send an email to license isb sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "cAMP regulates morphogenesis in the tungal pathogen Ustilago
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                                                                                                                                                        [1.83918; AAA57469.1;
                                                                        Repeat; Leurine repeat; CAMP synthesis; Magnesium
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ae: Ustiladinales: Ustiladinaceae: Ustilago
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POLY ALA.
                                          POLY ASP.
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                             LEDGINE RIGH REPEATS
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Hest Local Similarity 22.6
Matches 55; Conscivative
                                                                                                                                                                                                                                                                                                                                                                                                                                            b and anomalous behaviour of subunits a and b on polyacrylamide del electrophoresis in the presence of SDS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P10787;
01.JUL 1989 (Rel. 11, Created)
01.JUL 1989 (Rel. 11, Last sequence of
30 MAY 2000 (Rel. 89, Last annotation
HEMGGYANIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCYH PANIN
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                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS)
Gaykema W.P.J., Hol W.G.J., Verei)ken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Panulirus interruptus (California spiny lobster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1938 QLIDSDEFVIIANRTLWQYVSYQTA-----VDIARTQRNDPMIAAQKLRDFAISYGAE 1930
                                                                                                                                                                                                                                                 MEDLINE: 90064489.
                                                                                                                                                                                                                                                                                                                  "3.2-A structure of the copper-containing, oxygen Fanulitus interruptus haemocyanin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jekel P.A., Bak H.J., Soeter N.M., Verejken J.M., Beintema J.J.;
"Panulirus interruptus hemocyanin. The amino acid sequence of sabunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
Palinuroidea; Palinuridae; Panulirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                                                 "Crystal structure of hexameric baconcyanin from Panulirus interruntus retined at 3-2 A resolution.":
                                                                                                                                                                                                                                Volbeda A., Hol W.G.J.;
                                                                                                                                                                                                                                                                                                       Nature 309:23 29(1984)
                                                                                                                                                                                                                                                                                                                                                           Beintema J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                             Enr. J. Biochem. 178:403-412(1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECTION E.
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                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
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                                                                                                                                                        Mol. Riol. 209:249-279(1989).
FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
                           MISCELLANEOUS: THE B CHAIN CONTAINS TWO COPPER BINDING SITES
                                              SUBSTITUTION: EXTRACELLULAR TISSUE SPECIFICITY: HEMOLYMPH.
                                                                                 AND C HAVE BEEN IDENTIFIED
                                                                                                    SUBUNIT: HEXAMER OF A NUMBER OF DIFFERENT CHAINS, OF
                                                                                                                                       OPPURKING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLHSKS AND
           THREE HISTIDINE RESIDUES ARE LIGANDS TO EACH COPPER TON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.13
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2493 AA; 271979 MW; 106A872030105BFB 0R064;
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Pred. No. 16;
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PPAM: PPOUSTZ: homocyanio: 1.

PROMIE: PROUSTZ: homocyanio: 1.

PROSITE: PSOUZUS: HEMOCYANIO: 1.

PROSITE: PSOUZUS: HEMOCYANIO: 1.

PROSITE: PSOUZUS: IYROSINASE_2: 1.

PROSITE: PSOUZUS: IYROSINASE_2: 1.
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                                                                                                                                                                            ol-Aug-1992 (kel. 23, Created)
ol-Aug-1992 (kel. 23, Last sequence update)
ol-JUN-1994 (kel. 23, Last annotation update)
ENDOGLUCANASE C PRECURSOR (EC 3.2.1) (ENDO-1.4-BETA-GLUCANASE)
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Bacteria: Proteobacteria;
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HSSP; P04254; 1HCY
MEDILINE
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                                         SEQUENCE FROM N.A.,
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21.48;
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                                       AND SEQUENCE OF
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COPPER A.
COPPER A.
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Pred. No. 4.2:
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PEAM: PE02013: CBD_5: 1.
PEAM: PE00100: cellulase: 1.
PEAM: PE00150: cellulase: 1.
PROSTE: PS00561; CHD_BAGLEKIAL: 1.
PROSTE: PS00659: CLYCOSYL_HYDRO:_F5: 1.
CCllulose degradation: Hydrolase: Glycos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bit SWISS-PROL entry is copyright. It is produced through a coliaboration between the Swiss Institute of Biointonmatics and the EMBL outstation the European Biointormatics Hustitute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiochem: J. 279:793-799(1991).
-i- CATALYTH: ACTIVITY: ENDOHYDROLYSIS OF 1.4 BETA D-GIRCOSIDIC LINKAGES IN CELLULOSE. HACTERIAL-TYPE CELLULOSE-BINOING DERV
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INTERPRO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consists of multiple functional domains."; Biochem. J. 279:793-799(1991).
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"The cellodextrinase from Pseudomonas fluorescens subsp. cellulosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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$19652; $19652;
$197986; IEXH.
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1PR001919;
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SER-RICH (LINKER).
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5; Mismatches 111;
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0) NOV 1995 (Ref. 32, Last sequence update)
0) NOV 1995 (Ref. 32, Last annotation update)
(Soleher) TRNA SYNTHEIASE (BC 6.1.1.5) (ISOLEHEINE
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Proc. Natl. Acad. Sci. U.S.A.
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FORTALYTIC ACTIVITY: ATP + L ISOLEHICINE + TRNA(ILE)
PYROCHOSPHATE + L ISOLEHICYL TRNA(ILE).

FORTALTICE: HINUS ONE ZINC ION (BY SIMILARITY).

SHRUNTI: MONOMER (BY SIMILARITY).
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Panulirus interruptus haemocyanin.";
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Structure of panulirus interruptus hemocyanin and evolution of
arthropod hemocyanin, pp.33-62, Drukkeri) Van Denderen,
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Eukaryota: Metazoa: Arthropoda: Crustacea: Malacostraca:
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Gaykema W.P.J., Hol W.G.J., Verei)ken
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SUBCELLHEAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                                                           MOL. BIOL. 209:249-279(1989).
FUNCTION: HEMOCYANIN AKE COPPEK-CONIAINING OXYGEN CARKLERS
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SUMMARIES

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QUS.(1)
QUEER [1997] (THEMIGLOT, 02, Created)
Of FER [1997] (THEMIGLOT, 02, Last sequence update)
Of JAN [1997] (THEMIGLOT, 09, Last amoutation update)
Of JAN [1999] (THEMIGLOT, 09, Last amoutation update)
Of ACYLL D GLUCOSAMINE 2 EPIMERASE (BY 5.1. C.B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning and identification of N acyl b glucosamine epimerase from porcine kidney as a reninchinding protein."; J. Biol. Chem. 271:16294-16299(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A
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$4.6 OFROPEYGEMECYLNREGKVALTIKGGPFKGCFHVPRCLAMCEEMLSALLS
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85.0%; Pred. No. 2.6e 51
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Matches 140
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Sabmilled (MAK 1995) to the EMBL/SenHank/DDBJ databases
I. FUNCTION: CATALYZES THE INTERCONVERSION OF N ACETYLOLUGOSAMINE TO NEACHTYLMANNOSAMINE. HINDS TO RENTH FORMING A PROTEIN COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of MAY-2000 (TrEMHELGE, 18, Created)
of MAY-2000 (TrEMHELGE, 18, Last sequence update)
of JUN 2000 (TrEMHELGE, 14, Last sequence update)
of JUN 2000 (TrEMHELGE, 14, Last annotation update)
N ACTIGIDITIES AND INE 2-EPIMERASE (EC. 5.1.1.8) (GLCNAC 2-EPIMERASE)
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                                                                                             34 L HEADFEYGEWEGYLNRKGEVLLNLKGGKWKGCEHVPRALWLCAETL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KERETLQVMKKRVEQELDRVIAFMMEHSHIQEHGGFFTGLGRDGKVYDHLKYVMLQGRQV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FALHWAY: N.ACETYLNEDRAMINIC ACTO BE SUBBURIT: HOMODIMER (BY SIMILARITY).
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CATALYTIC ACTIVITY: N ACETYL D GLUCOSAMINE - N-ACETYL D
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                                                                                                                                 HGGLFYFQDADGFCFTQLEWNMKLWWPHSEAMIAFLMGYSDSGDPAILHLFYKVAEYTFR
                                                                                                                                                              FOSTFYFILDROGHPPOOLEWDOKLWWVHLETLVALAKGHQATGQEKCWOWFERVHDYAWS
                                                                                                                                                                                                                                VTPTGEFVDSFEGRLLNPGHGIEAMWFMMDIAQRSGDRQLQEQAI-AVVLNTLEYAWDEE 280
                                                                                                                                                                                                  VSEDGKELFGGLGRHQNFGHTLEAGWFLLQYALkKGDFKLRMH11DKFLLLFFHSGWDFE
                                                                                                                                                                                                                                                                     MMLLSLVEQLGEEDEELTNMYAELGDW----
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                                                                                                                                                                                                                                                                                                                                                                      SIMPAAMAFSQYALASGAQEAKATALQAYNNVLR-RQHNPKGQYEKSYPGTRPLKSLAVP 176
                                                                                                                                                                                                                                                                                                                                                                                                       WMYCKLYKSFEKERRVELLDAARAGGEELLRYAKVAPPGKKCAFVLIKEGRPVKVQRTIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                       WQFAVFYNRLE - PKPQWLEIARHGADFLARHGR - DQDGNWYFALDQEGKPLRQPYNVF 117
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419 AA;
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Pred. No. 8.5e 49;
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thi; Muridae; Murinae;
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Best Local Similarity
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17 (606) PRESIMINARY; PRI; 607 AA.
101-FEB-1997 (TrEMBLE-1. 02, Created)
101-FEB-1997 (TrEMBLE-1. 02, Last sequence up
101-JUN 2000 (TrEMBLE-1. 14, Last annotation)
                                                                                                   026180)
01-NOV-1996 (TrEMBLEDL 01, Created)
01-NOV-1996 (TrEMBLEDL 01, Last sequence update)
01-MAY-2000 (TrEMBLEDL 13, Last annotation update)
HEMOCYANIN PRECURSOR [CONTAINS: HEMOCYANIN, LONG FORM; HEMOCYANIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of the genome of the unicellular cyanobacterium Symechocystis sp. strain PCC6803. II. Sequence determination of the entire denome and assimument of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kuneko I., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hisosawa M., Sugiura M., Sasamoto S., Kimura I., Hisosawa A., Muraki A., Nakazaki N., Naruo K., Okumura S. Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHELICAL 70.0 KDA PROTEIN. SER1855.
                              Pendeus vannamei (Pendeid shrimp) (European white shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eurarida; Decapoda; Dendrobianchiata; Pendeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein SEQUENCE 607 AA;
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                                                                                        SHORT FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PKGQYEKSYPGTRPL-----KSLA--
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7; Mismatches
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PROPER
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PROSTIE: PS00498: PYROSINASE_2: 1.
Signal: Respiratory protein: Oxygen transport: Copper
Endoplasmic reticulum: Metal binding.
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HSSP: P04254: 11671.
INTERPRO: IPRODO896: -.
INTERPRO: IPROD2227: -.
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Sellos D.Y., Lemoine S., Van Wormhoudt A.;
"Molecular cloning of hemocyanin cDNA from Pendeus vannamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 15-52. TISSUE-HEPAIOPANCHEAS:
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METAI
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PROSTTE; PS00209; HEMOCYANIN_1;
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                                                                                            ERKSTESSVIVPDVPSTHDLFAHAHAG
                                                                                                                      QEKCWQWFERVHDYAWSH - FADPEYG 348
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22.5%; Pred. No.
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Rest Local Similarity
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                                         "Skibuga M., Zhang H., Endo A., Skishikula K., Kushiro I., Ebizuka Y., "Two branches of the imped synthese gene in the molecular evolution of plant oxide squarence syclasses,";
Eur. J. Ricchem. 266: 612 (07/199).
                                                                                                                                                                                                                                                01 MAY 2000 (TERMELET, 13, tast sequence update) 01 JUN 2000 (TERMELET, 14, tast annotation update) 14PE0L SYNTHASE (EC. 5.4.99.).
             EMBL: AB025443; BAAB6430; L; INTERPRO; TPRO01330; ...
                                                                                                                                                                              Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: Asteridae; cuasterids I: Lamiales;
                                                                                                                                                                                                                 olea europaea (Common olive)
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Walker M., Brooks S., Altati H., Aranjo R., Conn L., Conway
Conzelez A., Bansen N.F., Huizar L., Kremenetskaja I., Lenz
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Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
Magnoliophyta: endicotyledons: Rosidae; eurosids [1] Brassicales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN 2000) to the EMBL/GenBank/DDBJ databases. EMBL, Actol/944: AAF24989.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V.
Yu G., bavis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
"Genomic sequence tor Arabidopsis thaliana BAC F7F22 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F7F22.5.
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                                                                                                                 TESSUE LEAF;
                                                                                                                                SEQUENCE FROM N.A.
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20.3%; Pred. No. 1.2;
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                                                                                                      Wilson K., Ainscough K., Anderson K., Haynes C., Herks M.,
Rontield J., Button J., Connell M., Copsey L., Coopet J., Codson
Craxton M., Bear S., Du Z., Durbin K., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Loues M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Kifken L., Roopia A., Saunders D., Shawnkeen
Smaldon N., Smith A., Sonnhammer E., Staden K., Sulston J.,
Thierry Mied J., Thomas K., Vaudin M., Vanghan K., Waterston R.,
Watson A., Weinstock L., Wilkinson Specal J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
                                             Nature 368:32-38(1994).
EMBL: 793377; (ABO7572.1):
                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota: Metazoa:
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                PEAM: PFOUND43; GST;
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                            INTERPRO: IPROPOS21;
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                                                                                            "2.2 Mb of contiquous nucleotide sequence from chromosome
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 29970 MW;
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20.0%; Pred. No. 6.1;
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45EPHECHEDBAE912 CRC64;
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                                                                                                                                                                                                          ., Johnston L.,
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                                                                                             1111 04
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Matches 56
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PRINTS: PR00984: TRNASYNTHILE
PROSTIE: PR00178: AA_TRNA_LIGASE_I: 1.
Anningary1-trNA synthetase.
SEQUHENCE 1067 AA: 126108 MW: H7A8C
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL: AJ248285; CAB49833.1; -.
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INTERPRO; IPRO02300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holling R.;
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                                                                                                                                                                                             193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147
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                              CGHPPOOLEWDOKLWWVH---LETLVALAKG----HOATGOEKOWOWFERVHDYAWSHFA 34.3
                                                                EFKGREL - - EGLRYVHILMD - -
                                                                                            SFEGRELNPGHGTEAMWEMMDTAQRSGDRQLQEQATAVVLNTLEYAWDEEFGGTFYFLDR
                                                                                                                                                                                               EHEVRGEYKLRKDPSIYVKFPVEGKENEYLLIWTTTPWTLP----
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                                                                                                                                                                                                                                                              Similarity 20.4
56: Conservative
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PROKEFKEKYEWAHRVILADFVILEEGTGLVHTAPGHGE---
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                                                                                                                                                 ----EMEWILLPPHIVEEVILAQIVKEVMIDELDPETGLMREAVIPTGEEVD 230
                                                                                                                                                                                                                              -----EKSY------PGIRPLKSLAVPMILANLTL- - 184
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                                                                                                                                                                                                                                                                            4.3%;
20.4%;
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                                                                                                                                                                                                                                                                                                                                               126108 MW: B7A8C50C93924D82 CRC64;
                                                                                                                                                                                                                                                            c: Score : DB 1: Length 1067;
pred: No. 24;
24; Miss oches 47; Indels 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Mismatches 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                             -- ANLAVSAHP 242
                                                                                                                                ----KGEVVE
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--E 342
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                                                                                                                                             RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 057902;
01-ABG-1998 (TrEMBLiel. 07, Created)
01-ABG-1998 (TrEMBLiel. 07, Last sequence update)
01-MAY-2000 (TrEMBLiel. 13, Last annotation update)
HYPOTHETICAL 80.9 KDA PROTEIN.
             01-MAY-1999 (ITEMHLTEL 10, 01-JUN-2000 (ITEMHLTEL 14, 14, 14E14.10 PROTEIN, T4E14.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 392:353-358(1998).
EMML: AE000775; AAC07873.1; -.
INTERPRO: IPREOUB44; -.
PROSITE: PSOCI33; CARBOXYPEFT_ZN_2; UNKNOWN_1
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome of the hyperthermophilic bacterium Aquitex aeoficus.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILNE: 98196666.

MEDILNE: 98196666.

Decket G., Warten P.V., Gaasterland L., Young W.G., Lebox A.L.,

Graham D.E., Overheek R., Shead M.A., Keller M., Anjay M., Huker

Eeldman R.A., Short J.M., Olson G.J., Swangon R.V.;
                                                                             Q9ZVW2;
01-MAY-1999 (TrEMBLrel, 10,
                                                                                                             Q92VW2
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Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-VES;
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                                                                                                                                                                                                                         248 FMMDIAQKSGDKQLQEQAIAVVLNTLEYAWDEEFGGIF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 YDQAMILEAYIEGYQLLK-KDLFKQTVYEIVDFLKKDMLSPEGAFYSAWDADSEGEEGK: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 HNEMET.GRYYYRYKREQALKMIEKTE.FNMRMGGTYDHVGFGFHRYSTDREWILPHFEKMI 270
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                                                                                                                                                                                                                                                                                                                                                          PGTRPLKSLAVPMILANUITEMEWILLPPTTVEEVLAGIVR-----EVMTDFLDPEIGI.MK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEQNRQVWQFAVFYNRLEPKPQWLEIARHGADFLARHGRDQDGNWYFALD-----QEGKP-109
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                                                                                                                                                                                                                                                                                                                                                                                          692 AA; 80864 MW; 17CB4CDDAB972354 CRC64;
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Last annotation update)
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Best Local Similarity
Matches 60; Conserv
 Best Local Similarity
Matches 40; Conser
                            onery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              098W42;
098W42;
                                                                                                                                                                                                                                                                                                                            of MAY 2000 (TrEMBEREL 13, Created)
of MAY 2000 (TrEMBEREL 14, Last sequence update)
of JUN 2000 (TrEMBEREL 14, Last annotation update)
of JUN 2000 (TrEMBEREL 14, Last annotation update)
HYPOTHETICAL 44.5 KDA PROTEIN.
TILLELITO.
Albidopsis thaliana (Monse car cress).
FOKALYOLD VITIGIPLANTACE Emblyophyla: Flachcophyla:
ENKALYOLD VITIGIPLANTACE Emblyophyla: Clachcophyla:
Magnollophyla: endicotyledons: Rosidae; enrosids [1]:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robunstey S.D., Lin X., Kaul S., Shea T.P., Pujli C.Y., Mason T.M. Shen M., Roming C.M., Fraser C.M., Somerville C.R., Venter J.C., "Arabidopsis thatiana chromosome ILBAC TAEIA genomic sequence."; submitted (opt 1998) to the EMBL/GenBank/DBBJ databases.

EMBL; ACOUST/L: AAC6/203.1; ".

INTERPRO: IPRO01410; ".
                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (JUN 1999) to the EMBL/GenBank/DDBJ
EMBL; ALO79447; CAR45454.1;
                                                                                                                                                                                                                             Bevan M., Marphy G., Ridley P., Hudson S., Jesse T., Heijnen L.,
Vos P., Newes H.W., Mayer K.F.X., Lemeke K., Schueller G.;
Submitted (JBN 1999) to the EMBL/GenBank/DDBJ databases.
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Magnoliophyta; eudicotyledons; Rosidae; eurosids II;
                                                                                 SEQUENCE 391 AA;
                                                                                                                                                                                                                                                                                                           Brassicaceae; Arabidopsis.
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                                                                                                              PROSTIE; PSSOOOZ; PIPLC X,DOMAIN; L.
                                                                                                                                                                                                  SEQUENCE FROM N.A
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20.7%;
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               4.2%; Score 91;
24.0%; Pred. No.
                                                                                 MW.
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Pred. No. 7;
3; Mismatches
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                              DH 10;
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                                Length 391;
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Brassicales;
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Brassicales;
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44;
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Matches 49; Conserv
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01 NoV-1999
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01-MAY-2000 (TrEMBLIE). 13,
01-JUN-2000 (TrEMBLIE). 14,
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                                    CHRRAGO
                                             ORRAGO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and expression of chrysoptin, a salivary gland protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SALIVARY GLAND;
Leiner E.A., Reddy V.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO: IPR000934;
INTERPRO: IPR002224;
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                                                                                                          MKAWOEFVHEKGOEVVAESPVVLSKENCRVSLKINIGNEFFDAYVHEYVSSH
                                                                                                                                  CKLW
                                                                                                                                                        PVETVQTSGRKVLIVQASAFARYVGNITLYFDENNNLVRYAGAPVYLDSDVPQDPQTVEE
                                                                                                                                                                                                                                                     KGKYTKSVVLERGGRRIGIVGVIAQNTDNISSPGKLKFLDEIQSVKNESKRLREEEKVDI
                                                                                                                                                                                                                                                                             KGQYEKSYPGTRPLKSLAVPMILANLT-----LEMEWLLPPTTVEEVLAQTVREVMTDF 210
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                                                                                                                                                                      MMDTAGRSGERGT: - GEGGTAVVLNTT.EYAWDE: ---- EFGGTAYFTJERGGHPTGGTEWD
                                                                                                                                                                                                       VIVESHIGEDHDYDLAQQA - - - - GDY IDA I IG - - - - - GHSHSFLWTGENPPGKEKVVDDY
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                                                                                                                                                                                                                                                                                                                                                                                                                         PF01009;
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PS00785; 5_NUCLEOTIDASE_1; 1.
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                                                                                                                                 WVHLETLVALAKGHQATGQEKC - - - -
                                                                                                                                                                                                                                                                                                                                                            26
554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
           (TrEMBLrel.
                       (In EMBLiel.
                                                                                                                                                                                                                                                                                                     Conservative
                                                PRELIMINARY;
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Matches 49
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                                                                Merson Davies L.A., Condlitte E.;
"Analysis of live tylosin biosynthetic genes from the
the Streptomyces fradiac genome.";
Mol. Microbiol. 18:349-355(1994);
-!- SIMILARITY: HELGNGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                       SEQUENCE FROM N.A. SIRAIN-159235;
                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLIEL 01, Created)
01-NOV-1996 (TREMBLIEL 01, Last segmence update)
01-MAY-2000 (TREMBLIEL 13, Last annotation update)
CYTOCHROME P450 (EC 1.14.14.1).
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FROSTIE: PS00107; FROTEIN_KINASE_ATP; PKOSTIE: PS00108; PROTEIN_KINASE_ST;
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                                      EMBL; U08223; AAA21341.1; HSSP; Q00441; loxA.
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Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:
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Search completed: January 1, 2001, 22:57:47 Job time: 452 sec

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Copyright (c) 1993 - 2000 Compusen Ltd.
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SUMMARIES

Result No.	Score	Query Match	Query Match Length 198 - ID	ī	10	Description
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coprophorphyrinogen III oxidase; pantothenate synthetase; gene photosystem II Fel protein; polyA polymerase; regulatory components of sensory transduction system; renin-binding protein; sensory transduction bistidine kinase; serine acetyltransterase; tRNA-Ard; tRNA fe; tRNA ser; transposase; tymocyte protein chyzBKD; Allo3. Synechocystis sp. (strain:Perblod) DNA.	Symechorystis sp. BCC5803 complete genome, 14/27, 1719644-1848241. FOURLY AROUSE OF FOURLY	ENIS P	ACOO7545 Homo sapi AEOO 6617 brosophil AL355500 Homo sapi AL162712 Homo sapi ACO19153 Mus muscu U60056 Ralstonia e D26094 Flavobacter AL16494 Homo sapi	A 1027811 Homo Sapi A 1027847 Homo Sapi A 1027847 Homo Sapi A 1027847 Homo Sapi A 1027847 Homo Sapi A 1018634 Homo Sapi A 1018634 Homo Sapi A 1018635 Streptomy A 1018635 Homosculus A 1018635 Homosculus A 1018635 Homosculus A 1018636 Homoscu	CELESGA4 U53333 Caenorhabdi TITLE Sc CEC24F3 Al022716 Caenorhab S) AC010866 Hamo Sect S
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/note="ORF_ID:sll1256"
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COMPTEMBLE (4954 . .5545)
/note "ORF_ID:SII1258"
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GKRGVKENLVAGKKKGKKDLIAPMVFIGSLNAFFFEGNIKLYLLPSLDIPSILIMDNA
PIHRKIAIKELAKEAGHEVLFIFKYSPDLNDIEHDESALKRAKMYAPIDISLDEFIKS
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/db_xref="G1:1653235"
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/note-"ORF_ID:sIII257"
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/protein_id="BAA18149.1"
/db_xref-"G1:1653244"
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/product="H-/Ca2+ exchanger"
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/note="ORE_ID:sirl346"
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OROA I I AQKAQOMLEQLDPLSGEGI MYADLAKHYPSTLAAA I ALLNNEST "
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/protein id="hathis.1"
/db_xref="GI:1684/8"
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/db_xref-"601:1653-8 '5'
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complement(3551. .4623)
/note="ORF_ID:SIT|340"
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/note-"ORF_ID:s111255"
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proteins with reference to the function of the leucine zipper motif
J. Biochem. 110 (4), 493–500 (1991)
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/cell_type-"Wilms' tumor"
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Pred. No. 4.1e-29;
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Best Local Similarity 48.4%;
Matches 540; Conservative
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                                                                                           ACGGTACCAGAGCGAAGCGGTGGACATGATGGATCAGATCGTGCACTGGGTGCGAGAGGA
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Isukada,Y., Ohta,Y. and Maru,I.
Epimorase
Patent: US 5795767-A 9 18-AUG-1998;
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Maru, L. obta,Y., Murata,K. and Tsukada,Y.

Melecular cloning and identification of N acyl-b-glucosamine
& epimerase from porcine kidney as a renin binding protein
J. Riol. Chem. 271 (27), 16294 [6299 (1996)]
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NadeyE D glucosamine 2-epimerase.
Sus scrota (Strain:pEPFI) Kidney, cortex cDNA to mRNA,
Sus scrota
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Fig mkNA for N acyl-D glucosamine
ph 0766
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Submitted (OA MAK 1996) to the DDBJ/EMBE/GenBank databases.
Maru, Marukin Shoyu Co., Ltd., Kyoto Research Laboratories:
Monnemae, Todo, Uji, Kyoto 611, Japan
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Artiodactyla; Suitormes; Suina; Suidae; Sus.
1 (bases 1 to 1472)
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/rpt tamily "82"
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/protein_id "AAF22146.1"
/db_xret_"G1:6541050"
/evidence experimental
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/rpt family "METIR"
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07745, Germany
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    arbitrary, Gaps between the confids are represented as
    runs of N, but the exact sizes of the gaps are unknown.
    This record will be updated with the finished sequence.

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Insert size: 196814; 22.1% error; agarose tp.
Quality coverage: 1.74x in Q20 bases; sum of configs Quality
coverage: 1.26x in Q20 bases; agarose tp.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                      be presented.
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59961 60060: gap of 100 bp in length 60061 61087; condig of 1027 bp in length 61088 61187; qap of 100 bp 61188 64644 77617 74778 67290 69476; contiq of 2187 bp in length 69477 69576; dap of 100 bp 69577 710075 46.241 46.840; dap of 1028 bp in length 46.841 473.68; contid of 1028 bp in length 47.465 474.68; dap of 100 bp 474.69 501.55; contid of 26.87 bp in length 64645 64744; gap of 100 bp 64745 65998; contin of 1254 bp in length 84104 84004 81229 81328: dap of 76382 76481; gap of 100 bp 76482 77516; contig of 1005 bp in length 71928 72027; gap of 72028 74077; con 56209 56308: gap of 100 bp 56309 58154: contid of 1845 bp in length 53551 54650; gap of 100 bp 53651 56208; contid of 2558 bp in length 43270 19581 49680: qap of 100 bp 41882: contiq of 2202 bp in length 28659 34104 75x/x 77517 66099 65999 66098; gap of 58155 58254: 21815 51712 51811: 50256 43170 43269; gap of 41983 41883 41982; gap of 3744H 37547; 45.416 45415; gap of 100 pp 45.416 47447; contig of 2042 bp in length 34204 16323 16422; gap of 16423 17957; con 7417B 74078 50156 50255: 28559 28658: gap of 100 bp 28659 34103: contid of 5445 bp in Tength 18058 17958 18057: 14893 14793 14892: dap of 10751 10651 10750: dap of 12193-12292; gap of 7455 2293 8721 8820: 4576 4675; qap of 100 bp 4676 ____7 554; contid of 2679 bp in 7355 7454: gap of 83103: gap of 100 bp 85014: config of 1911 bp in length 74177: gap of 100 bp 76381: config of 2204 bp in length 85114: gap of 77616; gap of 34203: 4 1169: Contig of 1187 bp in length 83003; contig of 1675 bp in length 67189: contig of 1091 bp in length 46240: 71927; contiq of 2351 20: dap of 100 bp 10650: contid of 1830 bp in length 79777: contid of 2161 bp in length 53550: contid of 1739 bp in length 51711: 39580: 203: gap of 100 bp 35315: contig of 1112 bp in length 28558; contiq of 10501 bp in 16322: contid of 1430 bp in length 14792: 12192: contig of 1442 bp in length 8720: contid of 1266 bp in length 4575: contid of dap of dab of qap of gap of dab of qap of contig of 1535 bp in length Contid of contid of 1351 bp in length contid of 2050 bp in contig of 1456 bp in length contid of 2971 bp in length contiq of 2033 bp in length contiq of 2500 bp in length 100 bp 100 bp 100 bp 100 bp 100 bp laa bp 100 bp 100 bp luo bp 100 bp dq ool 100 bp 100 bp Too bp 100 bp loo bp low ty 2167 bp in length bp in length

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115184 115283; qap of
115284 118707; cont
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101446 107114; cont
107115 107214; gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-JUN-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestsanger.ac.uk
On Jul 16, 2000 this sequence version replaced qi:8573850.
                                        * consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the linished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                            Insert size: 150212; sum-of-contigs
Insert size: 159639; agarose-fp
Quality coverage: 2.85% in Q20 bases; sum-of-contigs quality
                                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-terminator Hig Dye: 100% of reads Consensus quality: 131709 bases at least Q40 Consensus quality: 138219 bases at least Q30 Consensus quality: 142824 bases at least Q20
                         * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: XGAP4; version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: bA344G16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
Contact: humquery sanger.ac.uk
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Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 154112)
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                                                                                                                                                                                                                                        coverage: 2.68x in Q20 bases; agarose-fp
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"assembly_fragment 95763		# CASH CALCANA				6" _fragment:	t_chain:5" .80969 assembly_tragment	t_chain:5" t_chain:5" .79781	γ_Iraqment	Traqment		+ T.S. (moon +	ragment .000			HOS7.	/note-"assembly_fragment:01120 fragment_chain:1"		9	/chromosome="13" /clone="RPLL-344316" /clone_lib "RPCL-11.2" 14426 /hote "assembly_fragment:00163	9061 149160: gap of 100 bp 9161 151795: contig of 2635 bp in length 1796 151895: gap of 100 bp 1896 154112: contig of 2217 bp in length Location/Oualifiers 1, 154112 /organism "Homo sapiens"

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MEDLINE
REFERENCE
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Matches 71; Conserv
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intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence comparison of the Caenorhabditis elegans dpy-13 and col-34 genes, and their deduced collagen products Gene 120, 261-266 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence comparisons of developmentally regulated collagen genes of Caenorhabdilis elegans
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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ilarity 57.7%;
Conservative
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99558, 102566
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97110. .99457
                                                                                                                                                     /codon_start-1
/product-%alpha-collagen%
/product-%alpha-collagen%
/protcin_id="AAA27985.1"
/db_xre1-%g1:156550"
/translation-"MOLETRIKAYRFVAYSAVAFSVVAVISVCVTLPMVYNYVHHVKR
                                                                                                                                                                                                                                                                                          Jegene="alpha-collagen"
join(585. .665,720. .1862,1411. .1583)
/qene="alpha-collagen"
join(585. .665,720. .1362,1411. .1583)
/qene="alpha-collagen"
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102667...109303
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95864. .97009
                                                PPGDSGEPGSPGLPGQDAAPGFPGPKGPKGPPGAPGAPGAPGAPGAPGAPGPAGPPLLPGEPG
PPGFAGPQGPPGSPGQPGATKSSPGQPGPKGPNGPDGQPGAPGAPGPAGPPGSPGE
                                                                                                        GPPGPAGTPGKPGRPGKPGAPGLPGNPGRPPQQPCEPTTPPPWKPCPQGPPGPPGPPG
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381. .393
                            RGICPKYCAIDGGVFFEDGTRR"
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/strain-"N2"
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Best Local Similarity 49.3%;
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                                                                                   Miller, N and Bradshaw, H.
The sequence of C. elegans cosmid F36A4
Unpublished (1996)
3 (bases 1 1-77)
                                                                                                                                                                                                                                                                                                              Latrellle,P., Lidhthing,J., Lloyd,C., McMurray,A., Mortimore,B., O'Calladhan,M., Parsons,J., Percy,C., Kilken,L., Roopra,A., Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sourhammer,E., Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaddin,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l (bases 1 to 42936)
Wilson, R., Ainscough, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans cosmid F36A4.
                 Submitted (01-APR-1996) Robert Waterston
                                                               Waterston, R
                                                                                                                                                                                                                                                     Wilkinson-Sproat, J. and Wohldman, P. 2.2 Mb of contiquous nucleotide sequence from chromosome
                                                                                                                                                                                                                                                                                        Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
                                                                                                                                                                                                                                                                                                                                                                                                  Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonfield, J., Burton, J., Connell, M., Copsey, J., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Khabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Caenorhabditis elegans
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                                         Direct Submission
                                                                                                                                                                                                              Nature 368 (6466), 32-38 (1994)
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/qene-"alpha-collagen
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Submitted by:
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Pred. No. 2.6;
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the program Genetinder(P. Green and L. Hillier, ms in preparation)
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| oin 19528 | 19611/9682 | 1971/9869 | 10197/10682 | 11199
| 11719 | 11224/12331 | 11311/13410 | 13853/14214 | 14954
| 15409 | 16997/17400 | 17607/18028 | 18213/19021 | 19122)
| Zaene "ama-1"
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/deno-"F46/
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/deno "F36A4.10"
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/complement(join(4926, .5098,5147, .5792,5847, .5927))
/product "C. elements DNA directed RNA polymorase II large substitute (ama 1) (SP:P16.69)".
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/protein_id="AAA96156.1"
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/db_xret_"G1:1255802"
/translation="MOLETICIKAYREVAYSAVAESVVAVISVCVTLEMYNYVHHVKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5140 AAAGATGITAIAGGTGACCTAFTITTAAAACTTGTCTTTCAGGACAACCCGGACCAAAGG 5081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
892 etygaalqggarraaaaqetetggtgggtacatttggaaaceetggttgceetagceaag 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    952 ggreareaugeeactggeaagaaa 976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101;
                             Direct Submission
Submitted (27-APR-1998) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RC, England and Department of Genetics,
Hinxton, Cambridge CB10 1RC, England and Department of Genetics,
Washington University, St. Louis, Mo. 63110, USA. E-mail:
jcs:sanger.ac.nk or rwenematode.wustl.edu
On Sep 22, 1998 this sequence version replaced di:3093277.
Coding sequences below are predicted from computer analysis, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erratum:[[published errata appear in Science 1999 Jan
1:283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 Sep
3:285(5433):1493}]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Scrience 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans cosmid C24F3, complete sequence
                                                                                                                                                                                                                                                                                                                                                                           McMurray, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The C.elegans Sequencing Consortium.
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predictions from Genefinder (P. Green, U. Washington), and other
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                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 14544)
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/protein_id-"AAA96163.1"
/db_xref-"G1:1255810"
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/protein_id="AAA95162.1"
/db_xre1="GI:1255809"
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/dene-"F36A4.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"F36A4.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KUHUKUSRUKPDEYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKVHKWVGHRRVKFLIDASANGKPKTCEWPFFYGGFWG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start-l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(31073. .31155,31211. .31304,31350. .31526)
/qene="F36A4.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MFEAEIDONIPGALWCGELYVLEQUVVFPDILRIDRFCISKSKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14544 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 30; Length 42936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neighbouring submissions. The true left end of clone 0.24\mathrm{F}3 is at 1 in this sequence. The true
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       overlapping sections once, or longer because we arrange for a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bin/display?db-wormacc&class-Sequence &object-024F3
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 281055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                once,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overlap between neighbouring submissions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the specified clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unambiquously on both strands, or on a single strand with both a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        It may be shorter because we only sequence overlapping sections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence is not the entire insert of clone C24F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPORTANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA
                                                                                                                                                                                                                                                                                                                                                                                      GDGTLESSDNVRTGFETGEELWSARSTNVRLAEQGVVDTMCNGSGSHHTLGKSNYRTNQ
LILGSSAKVGGVYLYANQRGCDGDRVYYDGASSVAQNGDLLAQTHQFDTEDTSVVSAV
VDLSDNQCFRHNKSSDKGNASDQVTVVPTRFDGKMTGGTKYNEKSTAPTHNVFDLQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MNQWDRRCRVATCTVNNWALDFKGNYEKIVKICEEAAALJAKIK
LGPELEIPGYGCADHEFELDTERHSWEMLSKLVEKSKKWPNLLVVTGLPTKERGLLYN
CAAALENGKLLFIRAKWCLADDNVYRESKWFVKWTETFKHYQMFLNSDIHFDQETVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA EST yk641
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(3350. .3553,3600. .4079,4128. .4203,
4336. .4433,5787. .5857,5907. .6021,6071. .6159,6204.
6420. .6764,6810. .6945,6997. .7231,7487. .7580))
/gene="C24F3.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(3350. .3553,3600. .4079,4128. .4203,4336. .4433,5787. .5857,5907. .6021,6071. .6159,6204.6420. .6764,6810. .6945,6997. .7231,7487. .7580))
                                                                                                                                                                                                                                                        GIFIDTIVTSILKVENVAYGEMPSEQSPDNRETMALQNIQARIRMVLSYLEAQLALVS
HKRPGGLLVLGTANVDESLVGYLTKYDCSSADINPIGSVSKKULRQFLEIAYEKYGMA
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                                                                                                                                                                                                                                                                                                                            TDGGDDPAYYLGGKKVGEDPAELCNQVLFTCYMASEHSSDETRQCAEGLAKNVNSSHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAN18773.1"
/db_xref="G1:3874484"
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/clone="C24F3"
/note-"predicted using genewise
                                                                                                                                                                DESYGEERTREKVVELKKNST"
                                                                                                                                                                                              LQLWGDKYSIDELEEKVNKFFWRYRVNRHKATVSIPAIHAENYSPDDHRNDHRPFLYP
                                                                                                                                                                                                                                                                                                                                                              PTAELCHGPPAYLWTYLKRSGMAGYFTPLSGGQDSSAVAAMVRLMCEKVCGATKKKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref~"SPTREMBL:Q9XXK6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"cDNA_EST_CEESW54F_comes_from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="C24F3.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Caenorhabditis elegans'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                     /qene-"C24F3.6"
                                                                                                  /qene-"C24F3.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .14544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST yk89h6.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST yk362d4.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST yk502q2.3 comes from this gene EST yk89h6.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yk641a2.5 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yk362d4.5 comes from this gene yk502g2.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yk259h4.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yk641a2.3 comes from this gene
                                                                .4834,4885.
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similar to CULICLE COLLAGEN 1 CDNA EST yk92d4.5 comes from this

cDNA EST yk92d4.3 comes from this

trite.

detie

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join(10845, .109
11600, .11799,111
/dene="C24F3,2"
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SNS
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                                                                                                                                                                                                                                       similar to boil specificity phosphatase, catalytic domain
cDNA EST yk4648.5 comes from this gene
cDNA EST yk452e5.3 comes from this gene
/Lianslation "MWKILENLYLAQLEMIVGETSKQEESKNDIKRVLILITTEPISEK
GKIGGVDYKFLHILIMFDEFILDNAILETAVLYINEGVEKEENVGVHGLAAVSKSVSI
CAAYLMYKNUWFVEKALKMIESVPKEIGPNAGFLAQLKIWEKSGMSESADQYKNLKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start_1
/protein_id="CAALB772.1"
/db_xref_"GL:8874483"
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CDNA EST yk448012.4 comes from this dene
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                                                                                                                     /protein id "CAAI877L]"
/db xref "GI:8874482"
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                                                                                                                                                                                  /conton start
                                                                                                                                                                                                                                                                                                                                /mote "predicted using denetinder
                                                                                                                                                                                                                                                                                                                                                               11600. .11799.1
Zdone "c24F3.2"
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/translation:"MVKPQ003KASKKPQPPILSHEFIIQNHGDIMSCVVMVFIVGLM
FPLHSUSSLFIAPQYNEIY LVAVEQ0QEREVHCYLS01LbLPATEFFXVCWIVVHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id "CAAlB/70.1"
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9213. (9554))
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Zdene "C24F3.1a"
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CALLAFIVFFERSHRR″
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VMHSDTVECKSEAGRIESGVNKTEPLIMMAHNKTARGAGEGNOGGEGGCTEGAGGDEGT
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/db_xref="dr:9367025"
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CDNA EST yk30215.4 comes from this gene"
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JOURNAL REFERENCE
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                                                                                                                                             AUTHORS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Washington, Po Hox (57730) Scattle, WA 98195, * NOTE: This is a 'working draft' sequence. It e
                                                                                                                                                                                                           Kowen,L., Madan,A., Qin,S., Abbasi,N., Batadarani,L., Birditt,B., Bloom,S., Bors,M., Dickhoft,R., Harrison,G., James,R., Lasky,S., Madan,A., Ratelitte,A., Shaffer,L. and Hood,L. Sequencina of human chromosome 15 D158160 p158115 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACO10866 115387 bp DNA HTG 25-SEP 1999 HOMO Sapiens chromosome 15 clone BACS 194N7 and 484G18 map 15q24.
*** SECTENCING IN PROGRESS ***, 98 unordered pieces.
                                           Submitted (25 SEP-1999) Multimedabase Sequencing Center, University
                                                                                                              kowen.L., Madan,A., Oin,S., Abbasi,N., Bar
Bloom,S., Dors,M., Dickhoff,K., Harrison,G
                                                                                                                                                                                     Oupablished
                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa: Chordata: Cianiata: Vertebrata: Enteleostomi;
Mammalia: Entheria: Primates: Catarrhini; Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                             Homo sapieus
                                                                          Direct Submission
                                                                                          Madan, A., Ratclitte, A., Shalter, T. and Hood, L.
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14438, 14544,28
/dene-"C24F3.3"
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complement(336...452), complement(168...288),
complement(105...119), complement(ALOZIS70.1:3682.
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RQTESEAADCTADY ERHEMMIA EGFEHEJIQKPURGSETRALIYAAVE FGQM ENFOKESC
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/Translation-*MLYTEQESTYFCLGYLLLFCKTSNAVKQSWEINQELFLEANKEH
TVFGDMRELQLRRESETAFSVLTPAQLTRYENSKDSDLSTRGVSHKGSSMNGWSNNTV
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/db_xref="G1:3874485"
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/codon_start-1
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'working draft' sequence.
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Search completed: January 1, 2001, 22:27:18 Job time: 18069 see

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ALIGNMENTS

RESULT S75649

renin-binding protein-related protein -N;Alternate names: protein slr1975 C:Species: Symethocystis sp. A:Variety: PCC 6803 Symechocystis sp. (strain PCC 6804)

C:Hate: 25-Apr-1997 *sequence_revision 25-Apr 1997 *text change 20-Jnn-2000 C:Accession: 875649 C:Accession: 875649 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996

A; Title: Sequence analysis of the genome of the unicellular eyanobacterium Synorb -7s

A;Reference number: \$74322; MUID:97061201 A;Accession: \$75649

A;Status: nucleic acid sequence not shown: translation not shown

A: Molecule type: DNA A; Residues: 1 - 491 - KAN-

A:Cross-references: EMH.:090912; GR:AHOULT39; NID:g1653228; PIDN:HAA18210.1; Fib:gir-A:Note: the nucleotide sequence was submitted to the EMHL Data Library. June 1996.

Опе Вез	Query Match 190.0%: Score 2147; 108-2; Length 391; Best Local Similarity 100.0%; Pred. No. 2.1e-176;	
Ma	Matches (91) Conservative 0; Mismatches 0; Indels 0; Caps	3
ζy	1 MIAHRRQELAQQYYQALHQDVLPFWEKYSLDHQGGGYFTCLDKKGQVFDTDKFIWLQNRQ 60	
Db	1 MIAHRRUELAQQYYQALHQDVLDFWEKYSLDRQGGGYET~LDRKGQVFDJDKFIWLQNRQ 60	
Оy	61 VWQEAVFYNRLEPKPQWLETARHGADFLAKHGRDQDGNWYFALDQEGKPLRQPYNVFSDC 120	
Db	61 VWUFAVEYNKLEPKEUWLEIARHGADELAKHGREUQDGNWYFALDUEGKPLRUPYNVESDC 120	
ç	121 FAAMAFSQYALASGAQEAKATALQAYNNVLRRQHNFKGQYEKSYPGTRFLKSLAVPMILA 180	
9	121 FAAMAFSQYALASGAQEAKATALQAYNNVLRROHNPKGQYEKSYPGTRPLKSLAVPHILA 180	
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361 LLNLKGGKWKGCFHVPRALWLCAETLQLPVS

301

DQKLMWVIILETLVALAKGIQATGQEKCWQWFERVIIDYAWSHFADFEYGEWFGYLNRRGEV DOKLWWYHLETLVALAKGHOATGQEKCWQWFERVHDYAWSHFADPEYGEWEGYLNERGEV

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300

181 NLTLEMEWLLPPTIVEEVLAQTVREVMTDFLDPEIGLMREAVTPTGEFVDSFEGRLLNPG

66.1 LLINILKOOKWKOOTEHVERALWIJOAKTIQILEVS

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A: Elle: Molecular cloning and sequence analysis of
A:Relectorece number: A45/41; MUID:90216621
A:Accession: A45/41
A:Status: preliminary
A:Molecule type: mRNA
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C:Species: Sus scrota demostica (demostic pig)
C:Date: 05 oct 1990 #seephence_revision 05-bet 1990 #text_change 05-Nov
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C:Species: Rathus micregious (Norway rat)
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C:Keywords: Uransmembrane protein
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J. Riol, Chem. 285, 688-6861, 1990
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  F:185 206/Region:
                             F:164 [B9/Region: hydrophobic
                                                           C: Keywords: leucine zipper
                                                                                   A:Cross references: GB:D1023: GB:D01086: NID:q220896; PIDN:BAA01083.1; PID:q220897
C:Comment: Renin binding protein is a protein that binds to renin to form a high molecu
                                                                                                                                                                                                                                                                 A: Fit be: Genetic and molecular properties of human
                                                                                                                                                                                                                                                                                            Rithode, H.; Takahashi, S.; Fukui, K.; Miyake, Y.
J. Biochem, 110, 498 500, 1991
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laucine zipper motif
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Query Match (1.1%) Score 668; DE 2; Length 419; Best Local Similarity (5.6%) Pred. No. 1.5e 49; Matches 145; Conservative 71; Mismatches 151; Indels 40;
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                                                                                                                                                                                                                                                                                                                                                                  87.2
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348 HOFRDPEYGEMFGYLNOEGKVALFTKGGPFKGCFHVPRCLAMCEOTL 394
                                                                                                                                                                                                                           280 EFGRIFYELDKORHPPOOLEWDOKLWWVHLETLVALAKGHQATGOEKCWGWEFEKVHDYAW 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 AVTETGEFVDSFEGRELNEGHGIEAMWEMMDIAQRSGDRQLQEQAI AVVLNTLEYAWDE 27s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 MMILINI. . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 SECEYTMAMNELWKVTGEMHYGREAVEMMEQTTHWVREDFAGLGREGGLSGTLATEFMAVE 182
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                                                                                   340 SHEADREYGEWEGYLNRKGEVLLNLKGGKWKGGEHVPRALWIGAETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 WMYSTKLYKLEEKKVELLDAAKAGGEFLLSYAKVAPPGKKSTAFVLLQESKFYKVQKLLE 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 RROELAQQYYQALHQD---VLPFWEKYSLDRQGGGYFTGLDRKGQVFDIDKFIWIQNRGV 61
                                                                                                                                                                            EHGGLEYEQDADDLCPTQLEWNMKLWWPHTEAMIAFLMGYRDSGDPALLNLFYQVAEYFF 347
                                                                                                                                                                                                                                                                                                                                                        NVSELGKELFGCLGRHQNPGHTLEAGWFLLQYALkKGDPKLQRHLIDKFLLLDFHSGWDF 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MILANIALEMENIAPPITVEEVIAQEVEEVMIDELDEEIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VEQLGEED- EEMIDKY-AELGDWCAHRILGHVQRDGGVVLE 227
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C:Accession: JX0188; G02510 Rainone, H.; Takahashi, S.; Fukui, K.; Miyake, Y. J. Hiochem. 110, 493-500, 1991 A:Fitte: Genetic and molecular properties of human and rat renim binding proteins wit A:Reference number: JX0187; MUID:92138649 A:Accession: JX0188 C:Species: Homo sapions (man) C:Date: 41 Mar 1992 #sequence_revision 31 Mar 1992 #text_change 20 Jun 2000. A: Molecule type: mRNA A: Residues: 1-417 · INO » remin-binding protein - human RRIDXU

Aptross-references: GB:D10242; GB:D01085; NID:q220052; PIDN:BAA01082.1; PID:q220054 R:Platzer, M.; Bauer, D.; Drescher, B. submitted to the EMBL Data Library, March 1995

A;Reference number: H01368 A;Accession: G02510

A:Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1:417 + PLA+

excomment: Renin binding protein is a protein that binds to renin to form a high A;Cross-reterences: EMBL:052112; NID:g1302657; PIDN:AAC51750.1; PID:g1302662

A;Gene: RbP Conetics.

A:Introns: 46/2; 61/4; 87/1; 144/3; 219/3; 247/1; 405/3; 449/4; 479/1 c:Keywords: Leuchne zipper E:164-149/Redion: hydrophobic E:185-206/Redion: Leucine zipper motif

Oberty Match 80.0%; Score 645; DB 2: Length 41 Best Local Similarity 84.7%; Pred. No. 1.4e 47; Matches 188; Conservative 75; Mismatches 163; Indets 5 RROELAQQYYQALIIQD++ VLPFWEKYSLDRQGGGYFTCLDRKGQVFDITbKFTWLQNROV-61

DB 2: Length 417;

3 KERETLOAMKERVOOELDRVVAEWMEHSHDOEHSIEFTETLIKREGRVYTEDLKYVMLOOROV 62

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A:Cross-references: EMBL:L19201; NID:q304961; PIDN:AAB03013.1; PID:g304984 A:Note: the uncleotide sequence was submitted to the EMBL Lata Library, October 1993 R:Blatther, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.: Rose, D.J.; Man R.; Shao, Y. Science 277, 1453-11-2, 1997 A:Ititle: the complete genome sequence of Escherichia coli K-12.

A:Reference number: Ab4720; MUID:97426617
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W.Alternate names: hypothetical protein t418
C:Species: Escherichia coli
C:Date: 19-May-1994 #Sequence_revision 01-Sep-1995 #text_change 04-Mar-2000
C:Accession: S40824; 255193
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C:Supertamily: Escherichia coli hypothetical 48K protein (qlnA-fdhE
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A:Accession: $40824
A:Status: preliminary; nucleic acid sequence not shown; translation not
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Nucleic Acids Res. 21, 3391-3398, 1993
A:Title: Analysis of the Escherichia coll genome. III. DNA sequence of the region
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A.Experimental source: strain K-12, substrain MG1655
C.Genetics
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A; Residnes: 1:418 - BLAL
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Best Local S
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IEIIEKYFWSEEEQMCLESWDEAFSKTEEYRG-----
                                                                                                                                                                                                                        FGWIRINKGOTKEEMGTHLWITAKMI.HVYSVA-----AAMGRPGAYSI.VDHG1KAM-87
                                                                                                                                                                                                                                                                      FTFTLDRKGQV_FDTDKFTWLONRQVWQFAVFYNRLEFKPQWLEJARHGADFLARHG----
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                                                                                                          NGALKDKKYOGWYACVNDEGVVDASKOGYOHF - - - FALLIGAAS - AVTIGHPEAKKELDYT 143
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                                                                                                                                                                 ----RDQD GNWYFALDQEG--KPLRQPYNVFSDCFAAMAFSQYALASGAQEAKAI----
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                      -ALQAYNNVLRRQHNPKGQYEKSYPGTRPLKSLAVEMILANLILEM 186
                                                                                                                                                                                                                                                                                                                                                             Score 148; DB 2;
Pred. No. 5.5e-05;
                                                                                                                                                                                                                                                                                                                                   Mismatches 186;
-GNANMHAVEAFLIVYDVTHDK 196
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R:Kaneko, T.: Sato, S.: Kotani, B.: Tanaka, A.: Asamizu, E.: Nakamura, Y.: Miyajima.
o, K.: Okumura, S.: Shimpo, S.: Lakeuchi, C.: Wada, L.: Watanabe, A.: Yamada, M.: Yas
DNA Res. 3, 109-136, 1996
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A.Varioty: nCC 6809
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20 Inn
C:Accession: 877092
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A:Accession: S77092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-607 < KAN>
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Best Local :
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                                                                                                                                                                                                                                                                                                    GEQKYADMLEYTEDT LEKYEPDY - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRLVYGFATAF-MMTGDDQFLEAAEKGTEYLREHMRFVDKDEDLIYWYHAIDVQGEKEQK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDADNKVI1KVWDGKQDIYHLLHCLVIPR 397
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ASAFYNAMFIDLEDGGTYFNVLANGTPYLAGG
                                                 ADPEYGEWEGYLNERG -
                                                                                                                                                                                                 NRAVVGHNIKTAWNIMRMNSI.KSKEKYVELAKKTADI.MPAVGSDGGRGGWYDVVERII.DN 4.28
                                                                                                                                                                                                                                                {\tt N---PGHGTEAMWEMMOTAQRSGDRQLQEQATAVVLNTLEYAWDEEFGGTFYFLDR--QG}
                                                                                                                                                                                                                                                                                                                                                   VEEVI.A-----QIVREVMIDELDPEIGLMREAVIPIGEFV------DSFEGRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEASEEGDDYDATPAYEGTYALAG-----PIQTYRCTGDRRILHDAEQTIKLEDKEE 269
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                                                                                              HSRCHQFVWHDRKAWWQQEQAILAYLILAGILDDEEYHRHGQE--
                                                                                                                                             HPP-QQLEW-DQKLWWVHLEILVA---LA----KGHQAIGQEKCWQWFERVHDYAWSHF 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -PKGQYEKSYPGIRPL----KSLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ERVRWP1VEAMGTAYALYTVTGDRQYETWYQTWWEYC1KYLMDYENGSWWQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.1%; Score 108.5; 22.7%; Pred. No. 0.2
                                               EVILLN- - - - LKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechocystis sp. (strain PCC 6804)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCFHVPR 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.22;
7; Mismatches 127;
                                                                                                                                                                                                                                                                                                    -DHSPFYQERFYEDWSHD1TWGWQQ
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A:Accession: 866003

A:Status: preliminary; nucleic ucid sequence not shown; translation not shown
A:Status: preliminary; nucleic ucid sequence not shown; translation not shown
A:Molecule type: DNA
A:Mosidnes: 1 ht; 'A',14 46,'A',38-54,'T',55-57,'WPSITKSPSITEKDNI,154,'S',156,'FKR' +032
A:Mossidnes: 1 ht; 'A',14 46,'A',38-54,'T',55-57,'WPSITKSPSITEKDNI,154,'S',156,'FKR' +032
A:Mossidnes: 1 ht; 'A',15 46,'A',38-54,'T',55-57,'WPSITKSPSITEKDNI,155,'FKR' +032
A:Mossidnes: 1 ht; 'A',15 46,'A',38-54,'T',55-57,'WPSITKSPSITEKDNI,156,'FKR' +032
A:Mossidnes: 1 ht; 'A',15 46,'A',38-54,'T',55-57,'WPSITKSPSITEKDNI,156,'FKR' +032
A:Mossidnes: 1 ht; 'A',15 46,'A',38-54,'T',55-57,'WPSITKSPSITEKDNI,156,'FKR' +032
A:Mossidnes: 1 ht; 'A',15 46,'A',15 46,'A
As Notes the nucleotide sequence was submitted to the EMBL Data Library, December 1993
ReKunst, F.: Ogasawara, N.: Moszer, E.: Albertini, A.M.: Alloni, G.: Azevodo, V.: Bert
C.: Bron, S.: Brouillet, S.: Bruschi, C.V.: Caldwell, B.: Capuano, V.: Carter, N.M.: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Ros. 1, 1:14, 1994
A:Title: Systematic sequencing of the 180 kilobase region of
A:Reference number: S65967; MUID:96051385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cibate: 28 oct 1996 #sequence_revision 13 Mar 1997 #text_change 20 Jun
CiAccession: 866006; 866003; C70085
Resonasawara, N.; Nakai, S.; Yoshikawa, H.
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A: Reterence number: $55.887
A: Access to no. $55.887
A: Molecule type: mRNA
A: Molecule type: mRNA
A: Mostiones: 16.62 - SEL
A: Access to the terences: EMBL: XBZ502; NID:qB54402; PIDN:CAA57880.1: PID:qB54403
C: SuperLamily: homocyanin
                                                                                                                                                                                                                                                                                                                                                                                                                                            Arctioss references: EMBL:026185; NID:q467326; PIDN:BAA05212.1; PID:q467366 A:Note: the nucleotide sequence was submitted to the EMBL bata Library, becember
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Cibate: 15 mil 1995 #sequence, revision 10
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Nature 39. 249-256. 1997

A.Authors: Foliare, D.: Fritz, C.: Fojita, M.: Fojita, Y.: Fuma, S.: Galizzi, A.: Galirethors: Foliare, D.: Fritz, C.: Foliar, M.: Fojita, Y.: Fuma, S.: Galizzi, A.: Galirethors: Latword, C.: Knoch, S.: Hilbert, H.: Holsappel, S.: Hosono, S.: Hollo, M. Koetter, P.: Koninostein, G.: Kroch, V.: Lee, S.M.: Levine, A.: Liu, H.: Masuda, S.: Man Y. M.: Guawa, K.: Gaiwara, A.: Ondega, H.: Fark, S.H.: Farro, V.: Fohl, T.M.: Fortete Rieger, M.: Schoeter, K.: Schoeter, Fark, S.H.: Farro, V.: Fohl, T.M.: Fortete Rieger, M.: Schoeter, K.: Scottoue, F.: Schouchi, J.: Sckowska, A.: Scakeuchi, M.: Lamakoshi, A.: Fanaka, F.: Forpstra, F.: Formoni, A.: Tosato, V.: Uchiya, M.: Minters, F.: Wipat, A.: Yamamoto, H.: Yamamoto, K.: Yasumoto, K.: Yasumoto, K.: Yasumoto, K.: Yasumoto, K.: Yoshikawa, H.: Danchin, A.: A.: Califitie: The complete denome sequence of the Gram positive bacterium Bacillus subtili A.: Accession: C700HS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Status: nucleic acid sequence not shown: translation not shown A:Molecule type: \ensuremath{\mathsf{DNA}}
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Nature 490, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.6%; Score 98.5; DE 2; Length 689; Hest Local Similarity 21.1%; Pred. No. 1.9; Matches 55; Conservative 47; Mismatches 100; Indels 59; Gaps
                                                                                                                                                                                                                                                                                                                                400 QLLKIREERIYPHYDDKYLTSWNALMIAGLAKAAKYYQEPKYLSLAKDALI - - - FIENK 455
516 DEEHGG-FYF: TGHDAEAL 532
                                                                          278 DEEFGGIFYFLDRQGHPPQQL 298
                                                                                                                                                             456 LIIIGKVMVKYKIGEVKNKGFIDDYAFLLWAYLDLYEASFDLSYLQKAKKLIDDMISLFW 515
                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 LASGAQEAKATALQAYN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 RYKE1CEQ11TFIQREMTHEDGSFFSALDADTEGEEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 LKTLGDOLGTLYCQVYD1TEEGNFEGKN1PNLIHTKREQ1KEDAGLTEKELSLKLEDAIQ 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 QWLEIARBGADELARBGROQDGNWYFALD-- - QEGKPLRQFYNYFSDCFAAMAFSQYA 130
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                                                                                                                                                                                                                                        NPGHGIE - AMWEMMDIAQRSGDRQLQEQAIAVVLNTLEYAW 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- NVLRKOHNPKOOYEKSYPOTRPLKSLAVPMILA 180
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A:Fitle: Purification of teline lysosomal alpha-mannosidase, A:Reference number: Z22083; MUID:98060744 A:Accession: I42219
                                                                                                                                                                                                                                             R:Berg, I.; follersrud, O.K.; Walkley, S.U.; Siegel, D.; Nilssen, O. Hiochem, J. 328, 863-870, 1997
                                                                                                                                                                                                                                                                                                                              alpha-mannosidase (BS 3.2.1.24) precursor, lysosomal - cat
C:Species: Fells silvestris catus (domestic cat)
C:Date: 26 Nov 1999 #sequence_revision 26 Nov 1999 #text change 26 Nov 1999
C:Accession: T42219
A; Cross-references: EMHL:AF010191; NID:q2804676; PID:q2804677; PIDN:AAH97672.]
                                                                            A:Status: preliminary
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                                                                                                                                                                                                       determination of its cbN
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68 LVAHTHIDDVGWLKTVDQYFYGTHNDVQHAGVQYTLDSVLSSLL

1 MIABERGED - - - - AQQYYQALHQDVIJEWEKYSLDRQGGGYETCIJDRKGQVETJIJKEIW 55

Onery Match 4.5%; Score 97.5; DB 3; Best Local Similarity 18.5%; Pred. No. 3.9; Matches 75; Conservative 51; Mismatches 155;

Conservative 51; Mismatches 155;

Indots 12%;

<u>=</u>

DPEFGTGAVK (SGDRQLQEQA
ALASGAQEAKATAL
QY 74 KPQWLETARHGADELARHGRDQDGNWYEALDQEGKPLRQDYNVESDGEAAMAESQY 129
UY 25 WEKYSIDROGAANFICHDRKGQVEDIDKFIWIONROVWGFAVFYNRLEP 73
Overy Match 4.4%; Score 95; DB 2; Length 876; Best Local Similarity 19.8%; Pred. No. 5.3; Mutches 74: Conservative 47; Mismatches 131; Indels 122; Gaps 18;
A:Residues: 1 876 (2012) A:Cross-references: (HAAL021246; GB:AL123456; NID:q3261507; PIDN:CAA16025.1; PID:q279148 A:Experimental source: strain H37Rv C:Genetics: A:Gene: vals C:Supertamily: valinetRNA ligase
A:Authors: Squres. R.; Sulston, J.E.; laylor, K.; Whitehead, S.; Barrell, B.G. A:Hitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A:Reterence number: A70500: MUID:98295987 A:Recession: G70864 A:Rolecule: preliminary; nucleic acid sequence not shown: translation not shown A:Molecule type: DNA
Cracression: CJO863 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Roders, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
RESULT 10 G70864 probable valS protein - Mycobacterium tuberculosis (strain H37RV) C:Species: Mycobacterium tuberculosis C:Lorens (7-101-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
CY 325K-WWWFERVIDYAWSHEALPEYGEWEGYLNRR 357 (:
QY Z68 VVLNILEYAMDEEEGGIFYFLDROGHPPOOLEMDQKLMWVHLETLVALAKG-HQATGQE- 325
CY 208 EDELDEEGLMKEAVIPTGEFYDSFEGRILNEGHGIEAMWEMMDIAQRSGDROLDEQAIA 267
QY 153 QHNPKGQYEKSYPGTRELKSLAVPMILANLTLEMEW LLPPTTVEEVLAQTVREVM 207 :
OY 102ALL-CEKPLROPYNVF-SDCFAAMAESOYALASGAOFAKATAL-DAYNNVL:RK 152 11
OY 56 LONROVWOFAVEYNKLEPKPOWLETARHGADELARHGKDO-DGNWYE 101 1:

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A:Molecule type: DNA
A:Residues: 1-2493 - GHL>
A:Cross-reterences: GB:L33918; NID:q603939; PID:q603940
A:Note: nucleotide sequence not given; amino acid sequence not complete
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adenylate cyclase (E. 4.6.1.1) uacl - smut fungus (Ustilado maydis)
C:Species: Ustilado maydis (corn smut)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09 Sep-1997
C:Accession: A55481
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A:Tille: CAME regulaties morphogenesis in the fundal pathogen Ustilago maydis A;Reference number: A55481; MUID:95087882
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A:Reference number: 219327
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A;Status: proliminary
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A:Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 QWFKAI 232
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E:1157 | H80/Lomain: leucine rich alpha 2 dycoprotein repeat homology (LRR2)

E:1287 | 1249/Lomain: leucine rich alpha 2 dycoprotein repeat homology (LRR4)

E:1287 | 1249/Lomain: leucine rich alpha 2 dycoprotein repeat homology (LRR6)

E:1386 | 1382/Lomain: leucine rich alpha 2 dycoprotein repeat homology (LRR6)

E:1386 | 1348/Lomain: leucine rich alpha 2 dycoprotein repeat homology (LRR6)

E:1380 | 1348/Lomain: leucine rich alpha 2 dycoprotein repeat homology (LRR6)

E:1380 | 1348/Lomain: leucine rich alpha 2 dycoprotein repeat homology (LRR8)

E:1380 | 1348/Lomain: leucine rich alpha 2 dycoprotein repeat homology (LRR8)

E:1380 | 1348/Lomain: leucine rich alpha 2 dycoprotein repeat homology (LRR8)
C:Keywords: coppet: alycoprotein; homolymph; oxyden carrier E:1 [75/Domain: 1, oncho ferminal abol: E:15/Domain: 2, oxyden binding abo2. E: 09 65/Zbomain: 3, carboxyl ferminal abod: E:09 65/Zbomain: 3, carboxyl ferminal abod: E:tatus experiment
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A.Fitle: Educilios interruptus hemoryanin. The amino acid sequence of subunit b and ano A.Fetlerence number: S02707; MUID:89091175
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                                                                                                                                                                                                                                                                                                                                                                                                                                      As Contents: annotations X ray crystallography, 3.2 and stroms As Note: the crystals contained a mixture of a and b chains; the structure was fit to a
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C;Species: Panulirus interruptus (California spiny lobster)
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J. Mol. Biol. 209. 18-279, 1989
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Ascentents: annotations X :
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Matches 55; Conservative 8
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A:Cross:references: EMBL:X61299
R:Ferreira, L.M.A.: Harlewhold, G.P.: Harker, F.J.: Gilbert, H.J. submitted to the EMBL Data Library, Advast 1991
A:Description: The cellodextrinase from pseudomonas fluorescence A:Reference number: S16849
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A:Residues: 1-262,'C',264-291,'K',293-748 <FE2>
A:Cross-reterences: EMBL:X61299; NID:q45501; PID:q45502
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C;Date: 14 Jan:1995 #sequence_revision 13 Jan:1995 #fext change 15 eet
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A;Status: preliminary
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A;Accession: $19652
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Biochem. J. 279, 794-799, 1991
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Best Local Similarity
Matches 71; Conserv
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455 SCSATNNPSSVTRIHAYDK --
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                                                                                                            RILDARPPYVDANKVGYDFTR
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344 343 arch com b time:	OY 231 SPEGRELINEGHOTEAMWEMMDTA - -	OY 153 QHNPKOQYEKSY	onery Match Rest Local Similarity 20.4 Matches 56; Conservative	A:Status: preliminary A:Molecule type: INA A:Rosidnes: F-1067 -KAW> A:Rosidnes: F-1067 -KAW- A:Rosidnes: F-1067 -KAW- C:Supertamily: IsolencinetRNA ligase	Rannonymous, Genoscope Rannonymous, Genoscope Submitted to the EMBL Data Library, A.Cosscription: Pyrococcus abyssi ge A:Acterence number: A75001 A:Accession: H75139	RESULT 15 H751 (9 Isoboucyl-tRNA synthetase (iles) PABU515 - Pyrococylisoboucyl-tRNA synthetase (iles) PABU515 - Pyrococylisobouc	UY 447 YGEWEGYLNEKGEVILNIKG E 1 1: 1: 1: 1: 1: 1: 1 Db 722 VIANDMWGGWTGFDPRKTOLLHNMWG	Db 674 CONTRACTION	QY 265 ATAVVEN -FLEYAWDEEPGGIPYF	Db 562 NEWGENTAEWEEN AND PARTIES.	VBBALLBANTAMBWLATAC 801 FOR AN ABALLBANTAMBWLTABLE 81 AN ABALLBANTAMBWLTABLBANTAMBWLTABLE 81 AN ABALLBANTAMBWLTABLE 81 AN ABALLBANTAMBWLTABBWLTABLE 81 AN ABALLBANTAMBWLTABBWL
ENERGERWRGEE 474YIEGKWRGIY 474 1, 22:54:19	ORSGDROLOEOATAVVLNILEYAWDEEFGGIFYFIDR	UHNIKGUY	4.48; Score 92; DB 2; Length 1067; 20.48; Pred. No. 14; dive 24; Mismatches 47; Indels 148; Gaps 14;	8285; CH:AL096836; NID:g5458067; PHDN:CAB49833.1; PID:g5458) In Orsay URNA Liquse	Library, July 1999 byssi genome sequence: insights into archaeal chromosome str	iles) PABU515 - Pyrococcus abyssi (strain orsay) i ce_revision 20-Ang-1999 #text_change 20-Jun-2000	SEVILINIKO 366 1:1 1: TOLLHNMMO 747	HLETI VALAKORQA I GOEKYWOWFEKVHDYAWSHFADDE	EPGBJEYFLDROGHPPOOLEW		-TLEMEWILLPHITVEEVIAOTVEEVMIDPILIPEIGIMREAVTPIGEFVDSF

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